

FIG. 1A

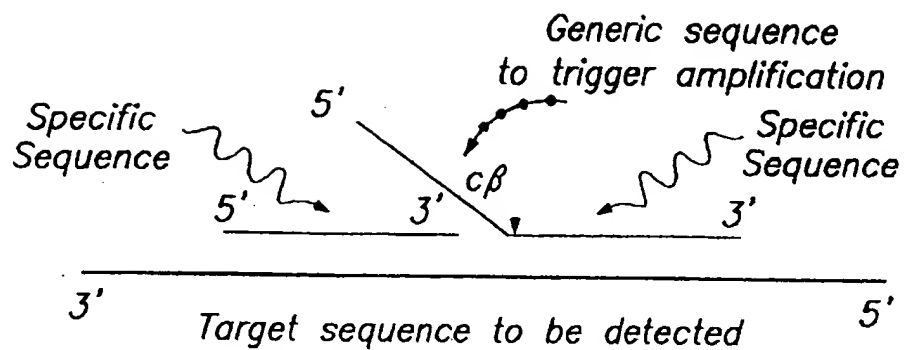


FIG. 1B PART ONE: TRIGGER REACTION

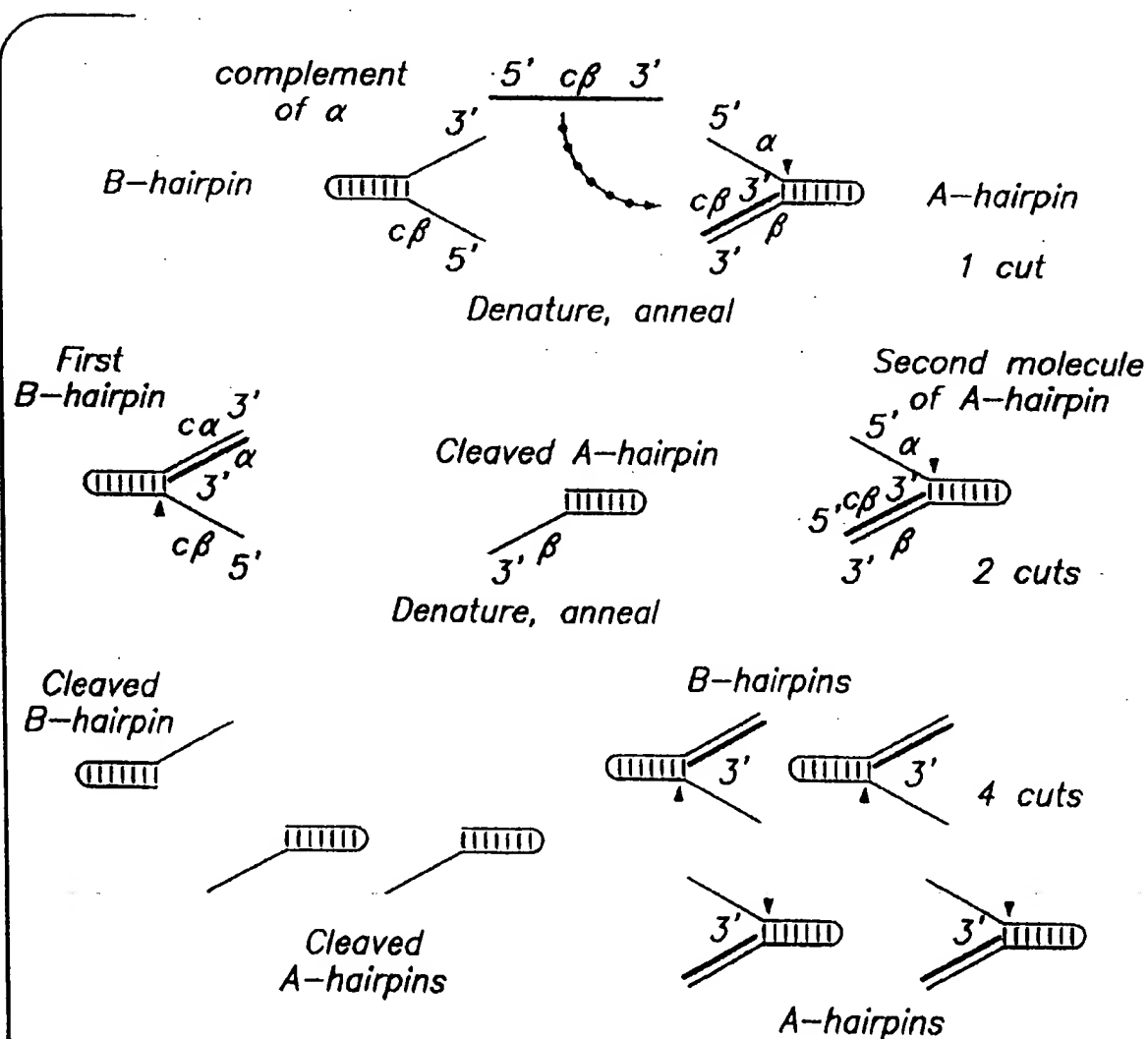


FIG. 1C PART TWO: DETECTION REACTION

FIG. 2A

MAJORITY [SEQ ID NO: 7]	ATGXGGGATGCTTGGCCCTCTTGAAGCCAAAGCCGGGTCTCTGCTGGAGGGCCACCACTGGCCCT	70
	AG..G.....G.....C..G.....	67
DNAPTAD [SEQ ID NO: 1]A.....	70
DNAPTFL [SEQ ID NO: 2]	GA.....G.....	
DNAPTTH [SEQ ID NO: 3]	
MAJORITY	ACGGACCTTCTTGGCCCTGAAGGGCTCAGCACAGCCGGGGGAACCGGTGAGGGGGTCTAGGGCTT	140
	CA.....G.....G..G.....C..T.....	137
DNAPTADG.....	140
DNAPTFL	
DNAPTTH	
MAJORITY	CGCCAAAGAGCCTCCTCAAGGCCCTGAAGGAGGACGGGACXXGGCGGIGXTGCTGGTCTTTGACGGCCAAG	207
A.....G.....GT..T.....	204
DNAPTADT..AA..G..CT..	210
DNAPTFL	
DNAPTTH	
MAJORITY	GGCGCCTCCTTGGGGCAGAGGGCTACGAGGCCTACAGGGCGGGCGGGCGGGCCGACCCCGGAGGACTTTC	277
G..GG.....GA.....G.....	274
DNAPTAD	280
DNAPTFL	
DNAPTTH	
MAJORITY	CGGGGACGCTGGGGCTCATCAAGGAGCTGGTGGACCTCCGAGGGCTTGGGGCTTGGGGCTTGGAGGTCCCGGGCTA	347
A.....T.....A..C.....	344
DNAPTAD	350
DNAPTFL	
DNAPTTH	

FIG. 2B

[illegible]

FIG. 2C

MAJORITY [SEQ ID NO:73]	TCCAGGCCCCACATCGAXGACCTGAXGCTCTCTCTGGAGGCTXTCCAGGCTGCCAGACCGACCTGCCCCCTGGA	
DNAPTAQ [SEQ ID NO:1]C..T...A.....C..GG..A.....	764
DNAPTFL [SEQ ID NO:2]GGG.....G.C...GCC.T...C..A...T...A...T.....	761
DNAPTTH [SEQ ID NO:3]	..A.....C...A...C.G.....T.....C...G.....C.....	770
MAJORITY	GGTGGACTTGGCCAGXGGGGGAGGGCGGACCGGAGGGGCTTAGGGCCCTTCTGGAGAGGCTGGAGTTT	
DNAPTAQAA.....A.....A.....T.....T.....	834
DNAPTFLGG.G.C.C.C.CACA...A...T...T...GG...T...T...C..T.....	831
DNAPTTHC.....C..G.....A.....C.....G.....C.....	840
MAJORITY	GGGAGCCCTCCTCCAGGAGTTCGGCCCTCCTGGAGGGCGCCGAAAGGCCCTGGAGGAGGCCCCCTGGCCCGCCGC	
DNAPTAQT.....AA.....	904
DNAPTFL	..A.....G.....G..G...GGCA.....T.....	901
DNAPTTHC.....C...GCC.....	910
MAJORITY	CGGAAGGGGCTTCGTGGGCTTGTCTTCGGGGCGGGAAGCCGATGTGGGGCGGAGCTTCTGGCCCTGGC	
DNAPTAQG.....AAG.....T.....	974
DNAPTFLT..TT.....TC.T...T.....	971
DNAPTTHC.....C.....G.....AAA.....	980
MAJORITY	CGCCGCCAGGGAGGGCGGGTCCAGCGGGCAGCAGACCCCTTTAXGGGGCTXAGGGAGCTXAAGGAGGTG	
DNAPTAQG.....C..C..G..T.A..AA.C...G.....C.....	1044
DNAPTFL	T.GG..GT.....G..CC...T.....A.....C...G...T...G...T...G...C...	1041
DNAPTTHTG.....C.....G.....GGC...G..A.A.....C.....C 1050	

FIG. 2D

MAJORITY [SEQ ID NO:7] GGGGGXCTGCTGGCCAAAGGACCTGGCGGTTTTGGCCCTGAGGGAAGGCGCTXGACCTCTTGGCCGCGGAGG

DNAPTAQ [SEQ ID NO:1]G..T.....A.....AG.....C.....A.....T.G.....CC.....C..... 1114
 DNAPTFL [SEQ ID NO:2]AA.....G.....G.....C.....C.....T.G.....A.A..... 1111
 DNAPTTH [SEQ ID NO:3]C.....C.....C.....TC.....G..A.....G..... 1120

MAJORITY ACCCATGCTGCTGGCTACCTGCTGGAGCCCTCGAACACGACGCCCGGAGGCGCTGGCCCGGCGCTACGG

DNAPTAQT..... 1184
 DNAPTFLT.....T.....T..... 1181
 DNAPTTHG.....G.....G..... 1190

MAJORITY GGGGGAGTGGACGGAGGAGXGCCGGGGGAGGGGGCGCTGCTXTCGGAAGAGGCTTCCXGAACCTXXGGAG

DNAPTAQG.....G.....G.....GC.....T.....GCC.....GTG..G. 1254
 DNAPTFLT.....A.....A.....GC.....A..C.....AAA.... 1251
 DNAPTTHC..C.CCC.C.....C..G.....CAT.G.....CCTTA.. 1260

MAJORITY CGCGTTGAAGGAGGAGGAGGCTGCTTGGCTTTACGAGGAGGTCGAGAGGCCCTTTCCCGGGTCCTGG

DNAPTAQA.G..... 1324
 DNAPTFLA...A..A..AC.C..G.....G.....G.....GCT..... 1321
 DNAPTTHC.....A.....A.....C.....C.....A.....C..... 1330

MAJORITY CCCACATGAGGGCGACGGGGGTGCGGCTGGAGGTCGGCTACCTCCAGGCCCTXTCCTGGAGGTCGGCGGA

DNAPTAQGG.....G..C.....G..C.....T...AG...T.G.....C... 1394
 DNAPTFLC.....C.....C.....C.....A..C 1391
 DNAPTTHC.....A.....A.....T.....T.....C.T..... 1400

FIG. 2E

MAJORITY [SEQ ID NO: 7]	GGAGATCCGCGCGCTCGAGGAGGAGGCTTCGCGCTGGCGGGGCGAGCCCTTCAAGCTCAAGTGGCGGGGAG	1464
DNAPTAQ [SEQ ID NO: 1]GC.....CG.....	1461
DNAPTFL [SEQ ID NO: 2]	...G.G...AG..G.....	1470
DNAPTTH [SEQ ID NO: 3]T.....G.....	
MAJORITY	CAGCTGGAAAGGGTGCTCTTTGACGAGCTXGGGCTTCGCGCGCATCGGCAAGACGGGAGAGACXGGCAAGC	
DNAPTAQG.....A.....	1534
DNAPTFLGC.....G.C..G..T.....	1531
DNAPTTHTA.....T.G..G.....C.A.....A.....	1540
MAJORITY	GCTCCAGCAGCGCGCGCTGCTGGAGGCGGCTXCGXGAGGGCCGACCCCATCGTGGAGAGATCCTGCCAGTA	
DNAPTAQG.....C.....C..C.....	1604
DNAPTFLT.....G..A.....CGGC.....	1601
DNAPTTHG.....A..G.....C.....C.....	1610
MAJORITY	CGGGGAGGTCAGCAAGCTCAAGAACACCTAGATXGACCCGCTGGCXGXGCTGGTCCAGCCCGAGGAGCGGGC	
DNAPTAQG.....G.....T.....G.A.....A.....	1674
DNAPTFLA.....C.C..G.....A..C.....	1671
DNAPTTHG.G.....C..AAG.....G.....	1680
MAJORITY	GGCGTCCACACCGCGCTTCAACGAGACGGGCCACGGCGGCGGCTTAGTAGCTCGGAGCCCAACCTGC	
DNAPTAQA.....A.....T.....C.....	1744
DNAPTFLG.....C.....TCC.....	1741
DNAPTTHG.....G.....	1750

FIG. 2F

MAJORITY [SEQ ID NO:7]	AGAACATCGCGGCTCGGACGCGCCXCTGGGCGCAGAGGATCGGCGCGGCGCTTCGTGGCCGAGGAGGGGTGGGT	
DNAPTAQ [SEQ ID NO:1]G..T..G.....A..C.....G...C..	1814
DNAPTFL [SEQ ID NO:2]G.....T.....C..C.....A.....C.....	1811
DNAPTTH [SEQ ID NO:3]CT.....C.....T.....C.....T.....C..	1820
MAJORITY	GTGGTGGGCTGGACTATAGCCAGATAGAGCTCGGGGTCTGGCGCGGCGCTCTCGGGGACGAGAACCTG	
DNAPTAQ	A.....T..T.....C.....A.....G.....C.....	1884
DNAPTFL	C.....T..T.....C.....T.....T.....T.....	1881
DNAPTTHC.....C.....C.....C.....A.....	1890
MAJORITY	ATCGGGGTCTTCAGGAGGGGAGGACATCCACACCCAGACGGCGAGGTGGATGTTGGGGTCCCCCGGG	
DNAPTAQG.....G.....G.....G.....G.....G..	1954
DNAPTFLT.....T.....T.....T.....T.....T..	1951
DNAPTTH	A.....A.....A.....A.....A.....A.....	1960
MAJORITY	AGCGCGTGGACCCCTGATCGCGCGGCGGCCAAGACCATCAACTTCGGGGTCCCTCTACGGGCACTGTCGGC	
DNAPTAQA.....T.....T.....T.....T.....T.....G..	2024
DNAPTFL	A..GG..A.....T.....T.....T.....T.....G.....	2021
DNAPTTHGG..GG..GG..GG..GG..GG..C.....C.....	2030
MAJORITY	CCACCGGCTCTCGCAGGAGCTTGGCCATCCGCTACGAGGAGGGGGTGGCCCTTCATTGAGCGGCTACTTCCAG	
DNAPTAQA.....T.....T.....T.....T.....T.....T...	2094
DNAPTFLGG.....T.....T.....T.....T.....T.....	2091
DNAPTTH	...TA..G.....T.....T.....T.....T.....T.....A	2100

FIG. 2G

MAJORITY [SEQ ID NO:73]	AGCTTCCCAAGGTGCGGCGCTGGATTGAGAAAGACCCCTGGAGGAGCGGCGGCGGTACGCTGGAGGA	2164
DNAPTAQ [SEQ ID NO:17]	2161
DNAPTFL [SEQ ID NO:27]	A.....GG.....C.....C.CC.....T.....	2170
DNAPTTR [SEQ ID NO:37]A.A.....G.....A.....C.....A.....	
MAJORITY	CGCTCTTGGCGCGCGCGGTACGTGCGCGGAGCTCAAGCGCGGGTGAAGAGCGGTGCGGCGGAGCGCGCGGA	
DNAPTAQC.....A.....AG.G.....C.....	2234
DNAPTFLT.....C.....	2231
DNAPTTRAA.AA.....CA.....C.....	2240
MAJORITY	GGGCAATGGCCCTTCAACATGCGCGTCCAGGCGCAGCGCGCGGACCTCATGAAGCTGGCCCATGGTGAAGCTC	
DNAPTAQG.....T.....	2304
DNAPTFLG.....CG...T	2301
DNAPTTRC.....C.....	2310
MAJORITY	TTCGCGCGCGCTXCAGGAAATGGGCGCCAGGATGGTGGTXCAGGTCGACGAGCGAGCTGGTCCCTCGAGGGCCC	
DNAPTAQA...GG.....T.....	2374
DNAPTFLT.....C.....G.....TT.G.....G.....	2371
DNAPTTRC.C.G...G.....C.C.....C.....G.....	2380
MAJORITY	CCAAAGAGCGGCGGAGCGXGGTGGCGCGCTTGGCCCAAGAGGTCATGGAGGGGCTCTATCCCCCTGGCCCGT	
DNAPTAQ	A.....A.....CC.....CGGC.....G.....	2444
DNAPTFLG.C.....AG...A.....GG.....CAG..	2441
DNAPTTRC...C.....C...A.....G.....C.....AA..C.....C.....	2450

FIG. 2H

MAJORITY [SEQ ID NO:7]	GGCCCTGGAGGTGGAGGTGGGGATGGGGGAGGACTGGCTCTCGGGCCAAAGGACTAG	
DNAPTAO [SEQ ID NO:1]A.....	GA 2499
DNAPTFL [SEQ ID NO:2]CC.....	2496
DNAPTTH [SEQ ID NO:3]T.....GT...	2505

FIG. 3A

MAJORITY [CSED ID NO:8]	MXAML PLFEPKORVLLVDGHHLAYRTFFALKGLTTSRGEPPQAVYGFAXSLLKALKEDG-DAVXUVFQAK	
TAD PRO [CSED ID NO:4]	RG.....H.....	69
TFL PRO [CSED ID NO:5]V.V.....	68
TTH PRO [CSED ID NO:6]	E.....YK..F.....	70
MAJORITY	APSRHEAYEAYKAGRPTPEDFPROLALIKELVDLLGLXRLEVPQYEADDDVLA TLAKKAEKEGYEVAIL	
TAD PRO	GG.....A.....S.....	139
TFL PROV.....F.....R.....	138
TTH PROFT.....	140
MAJORITY	TADRDLYQLLSDRIAVLHPEGYLITPAWLWEKYGLRPEQWVDYRALXGDPSONLPGVKSI GEKTAXKLLX	
TAD PRO	K.....H.....D..A...T..E.....R...E	209
TFL PROE..I.....Y.....A.....I.....OR..IR	208
TTH PRO	V...V...H...E...F...V.....L...K	210
MAJORITY	EWGSLLENLLKNLBRVKP·XXREKIXAHMEDLXLSXXLSXVRTDLPLEVDFAXRREPDRGLRAFLERLEF	
TAD PRO	A.....L...AI...L...D..K..WD.AK.....K.....R.....	278
TFL PROFQH..Q...SL...LQ.G..A.A..RK..Q.H.....GR..T.NL.....	277
TTH PROENV...K..L...R..LE..R.....L.OG.....	280
MAJORITY	GSLLEHFGLEXPKALEEAPWPPEGAFVGFVLSRPEPMHAE LLALAAARXGRVHBRAXDPLXGLRDLKEV	
TAD PROS.....K.....D.....G.....PE.YKA.....A	348
TFL PROG...A.....L..SF.....G.WE..L...Q...R.....G.	347
TTH PROA.AP.....K.....C.D.....A...A..K.....	350

FIG. 3B

MAJORITY [SEQ ID NO: 8]	RGLLAKOLAVLALREGDLXPCDDPHMLAYLLDPSNTTPEGUARRYGGEWTEGAGERALLSERLFXNLXX	
TAQ PRO [SEQ ID NO: 4]	S.....G.P.....E.....A.....A.....WG	418
TFL PRO [SEQ ID NO: 5]	I.....F.E.....A.....OT..KE	417
TTH PRO [SEQ ID NO: 6]	S.....V.....AH.....HR..LK	420
MAJORITY	RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLOALSLEVAEEIARLEEEVFRLAGHPFNLNSRD	
TAQ PRO	R...R...A.....R.....A.....A.....	488
TFL PRO	K.....E.....R.....EA.V.Q.....	487
TTH PRO	K.....H.....L.....	490
MAJORITY	QLERVLFDELGLPAIGTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTCLKNTYIDPLPXLVHPRTG	
TAQ PROS.....D.I.....	558
TFL PRODR.....A.....K..	557
TTH PRO	R...L...Q.....H.....V.....S.....	560
MAJORITY	RLHTRFNQTATGRLSSSDPNLQNI PVRTPLGQRI RRAAFVAEEGWXLVALDYSOIELRVLAHLSQDENL	
TAQ PROL.....L.....	628
TFL PROV..V.....	627
TTH PROA..A.....	630
MAJORITY	IRVFQEGRDIHTQTASWMF GUPPEAVOPLMRRAAKTINFGVLYGMSAHLSDQLAI PYEEAVAFIERYFO	
TAQ PRO	E.....R.....Q.....	698
TFL PRO	S..G.....G..S.....	697
TTH PRO	K.....V.....	700

FIG. 3C

MAJORITY [SEQ ID NO:8]	SFPKVRAWIEKTL EGRRRGYVETL FRRRYVPDLNARVKSUREAAERMAFNMPVGGTAADLMK LAMVKL	768
TAQ PRO [SEQ ID NO:4]E.....	767
TFL PRO [SEQ ID NO:5]	Y.....G.....R.	770
YTH PRO [SEQ ID NO:6]K.....	
MAJORITY	FPRLXEMGARM LQVHDELVL EAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX	
TAQ PROE.....E...A...R.....I.....	833
TFL PROO.L.....D...R.....W..O...L.....	831
YTH PROR.....L.....QA...E.....A..KA.....M.....G	835

Genes for Wild-Type and Pol(-)DNAPTaq

Domain
Coding Regions: 5' Nuclease

Polymerase

FIG. 4A

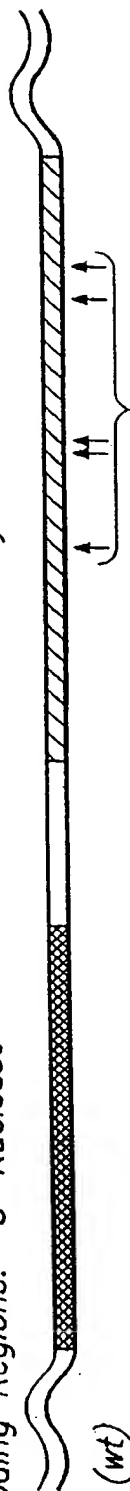


FIG. 4B

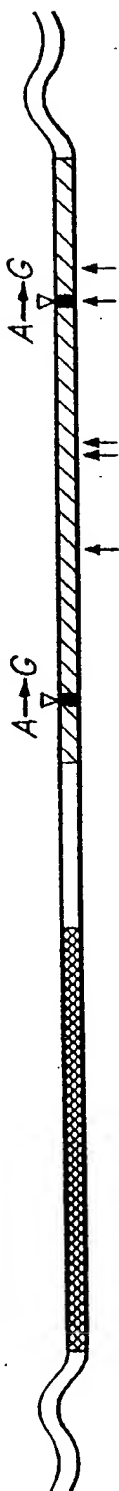


FIG. 4C



FIG. 4D

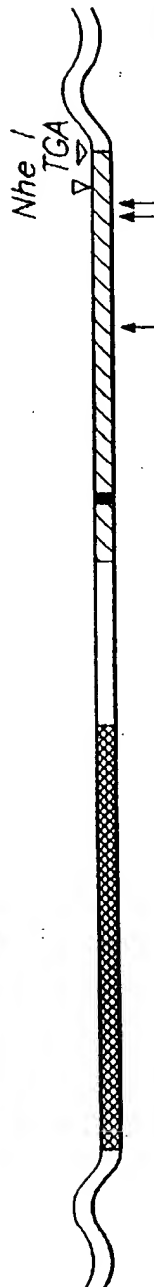


FIG. 4E



FIG. 4F

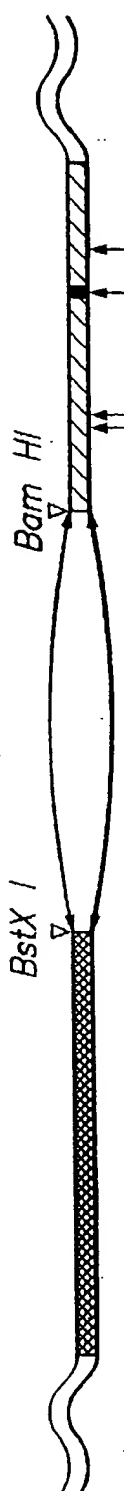


FIG. 4G



Genes for Wild-Type and Pol(-) DNAPTfl

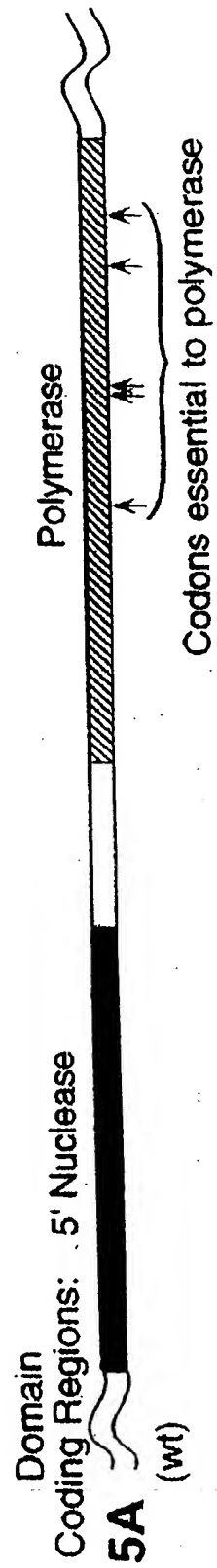


FIG. 5A

(wt)



FIG. 5B

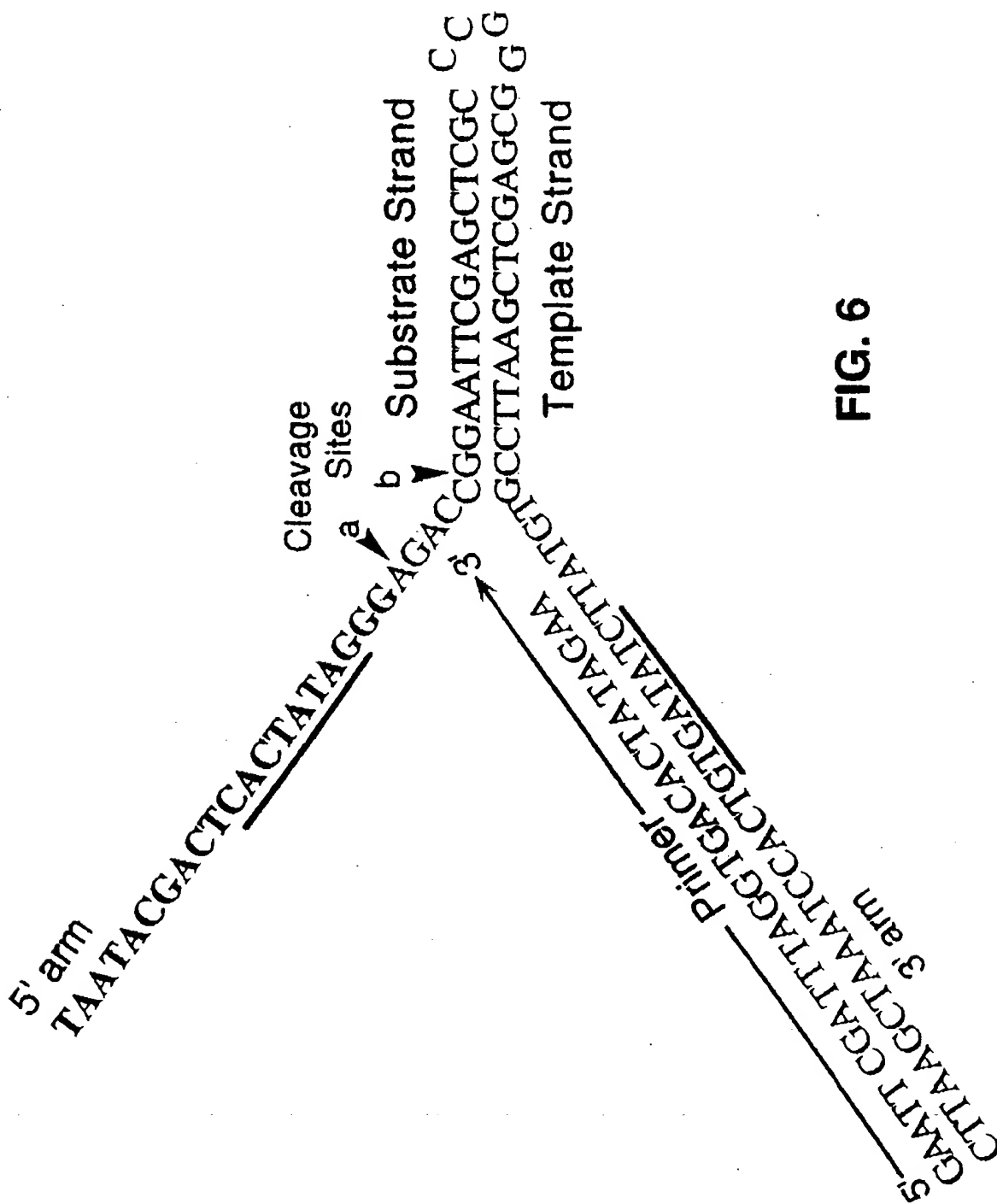


FIG. 6

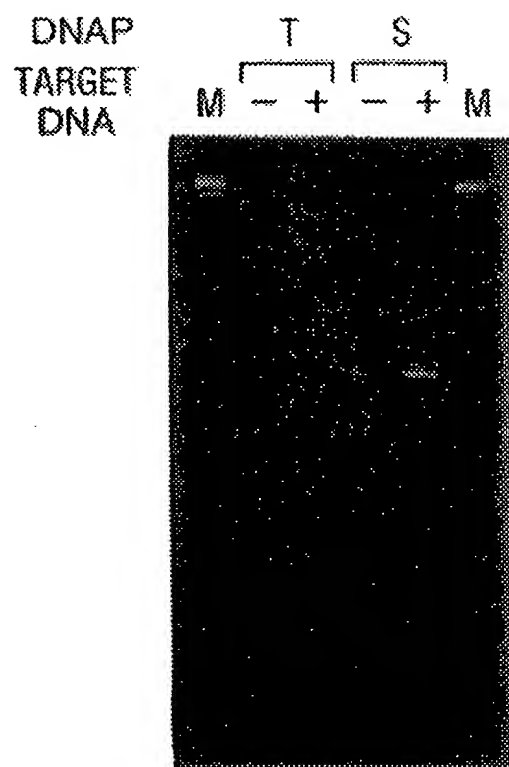


FIG. 7

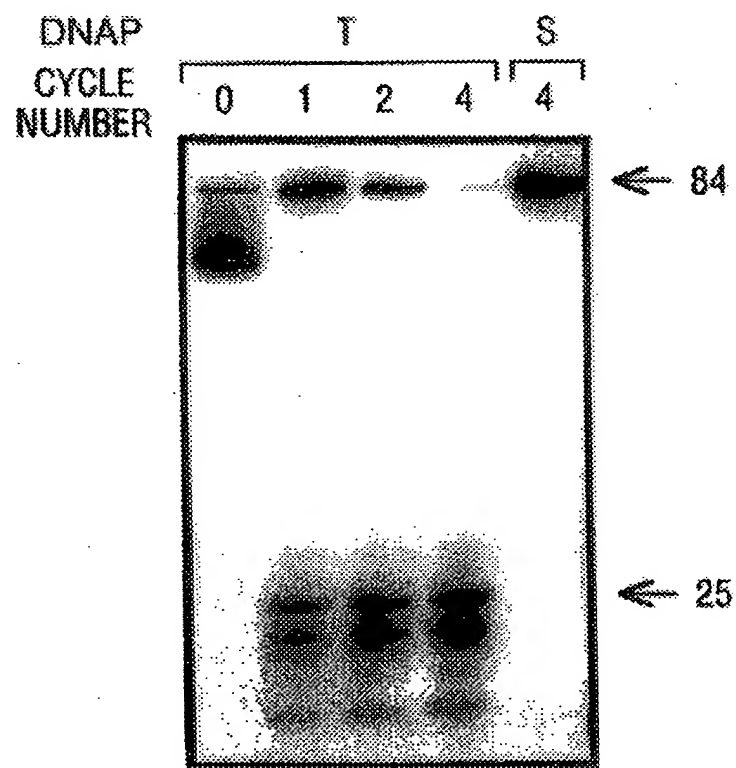


FIG. 8

	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl ₂ :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

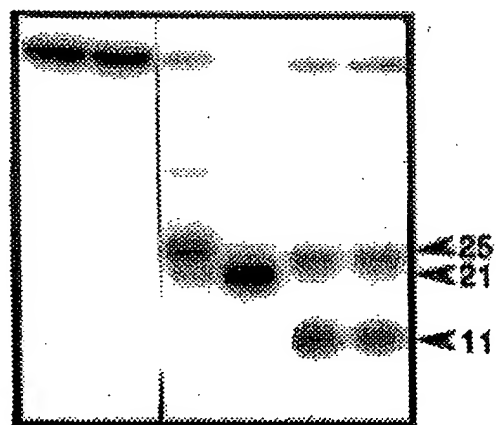


FIG. 9A

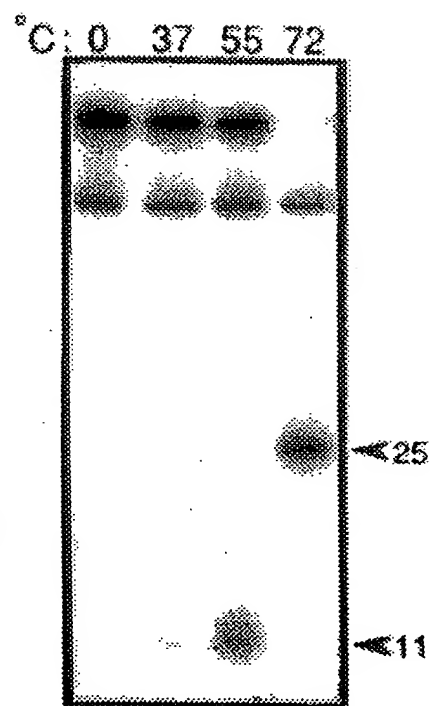


FIG. 9B

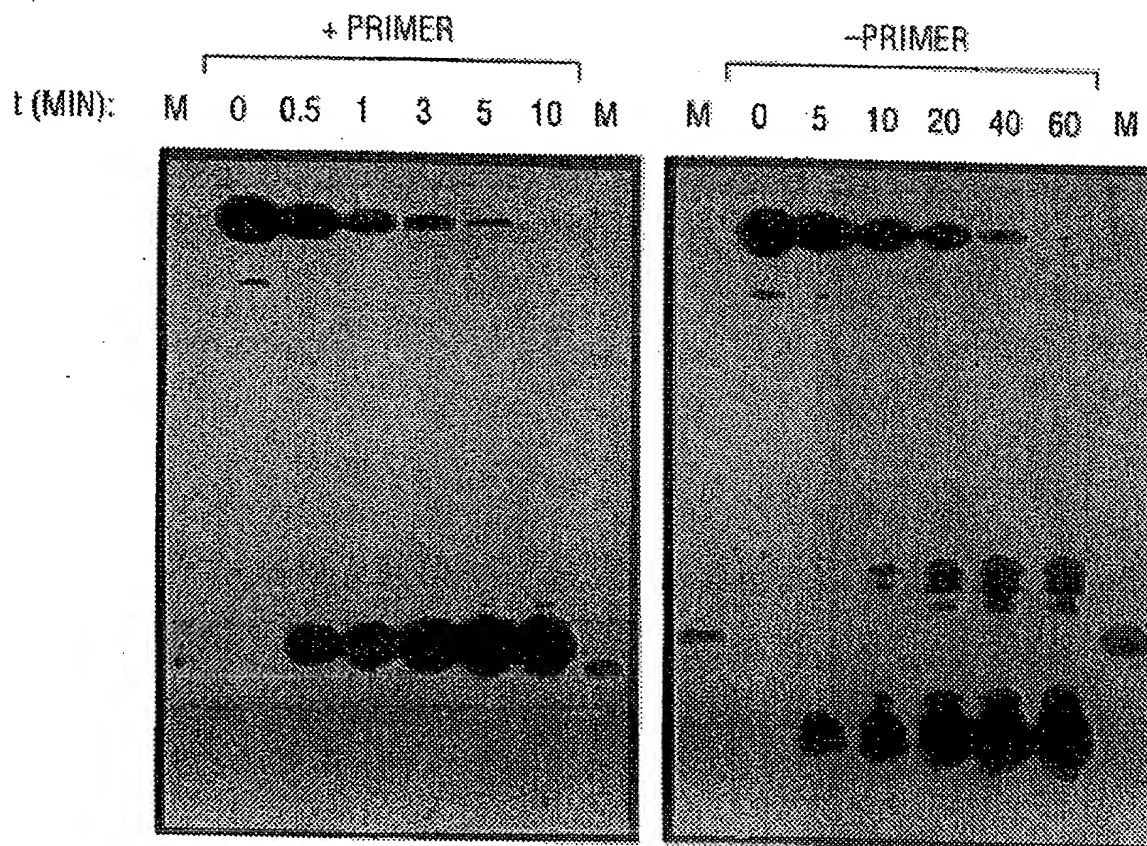
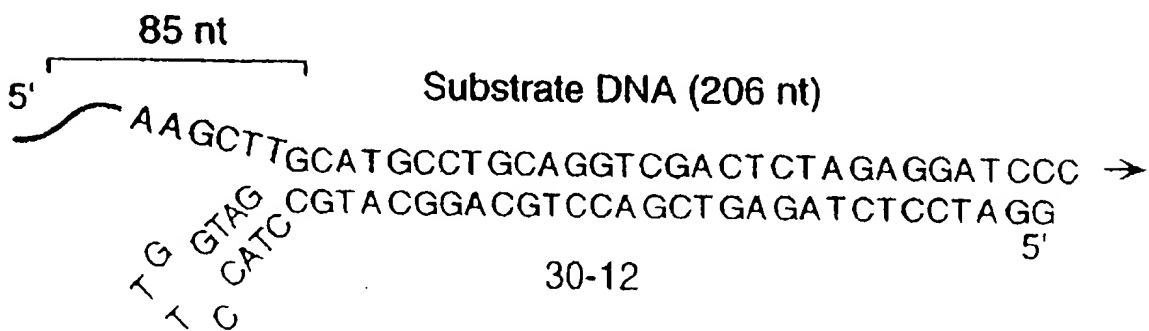
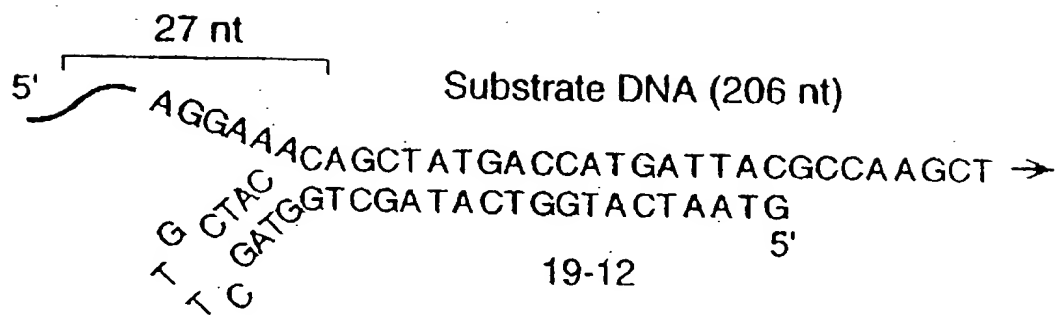


FIG. 10A

FIG. 10B



FIG. 12A



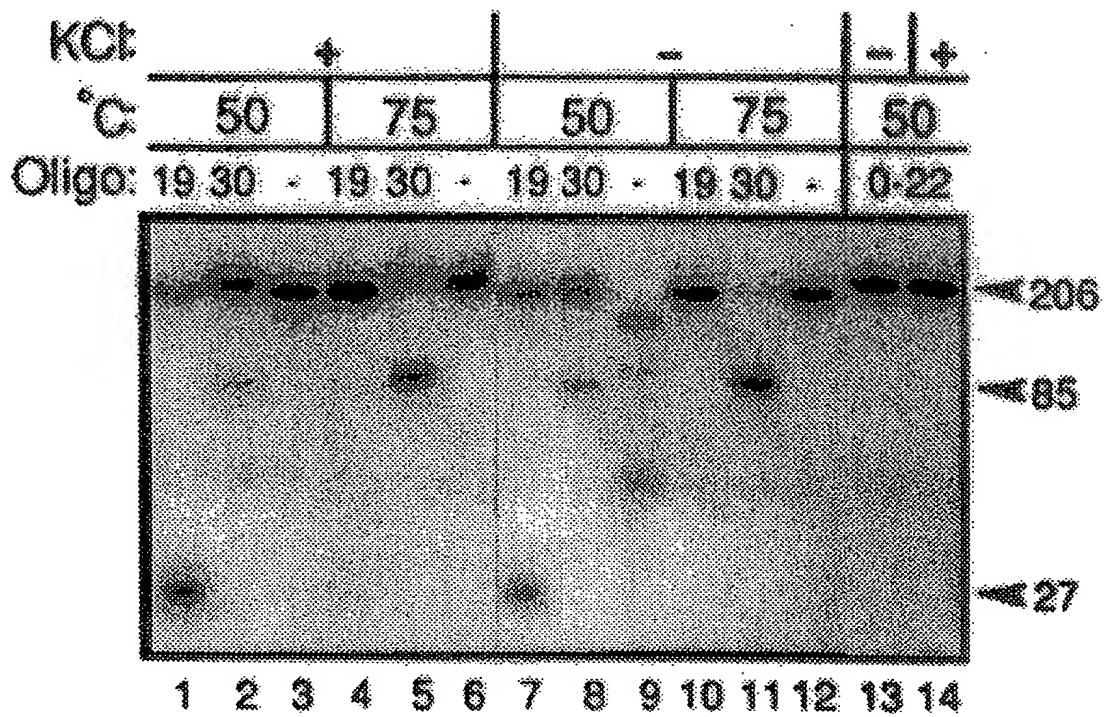


FIG. 12B

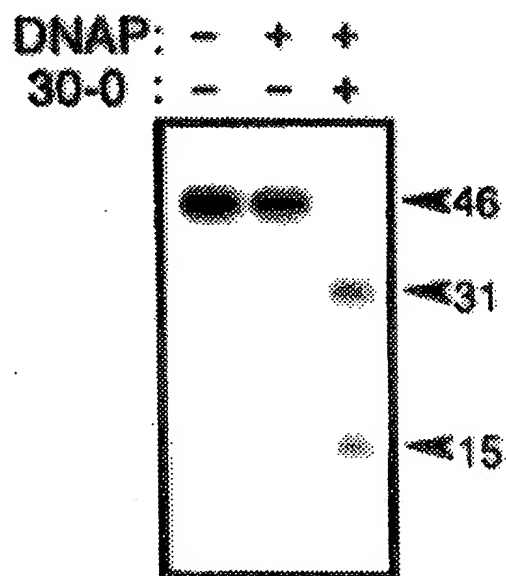


FIG. 13B

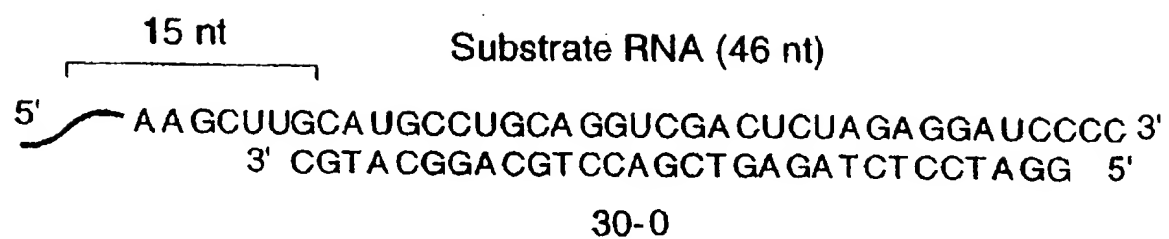


FIG. 13A

-35 -10 RBS
 TTGACAATTAATCATCGGCTCGTATAATGTTGTGGAAATTGTGAGCGGATACAATTTACACAGGAACAGCG
 MetAsnSer...
 ATGAATTCGAGCTCGGTACCCGGGATCCTCTAGAGTCGACCTGCAGGCATGCAAGCTTGGCACTGGCC
 EcoRI KpnI BamHI Sall PstI SphI HindIII
 SstI SmaI XbaI

FIG. 14B

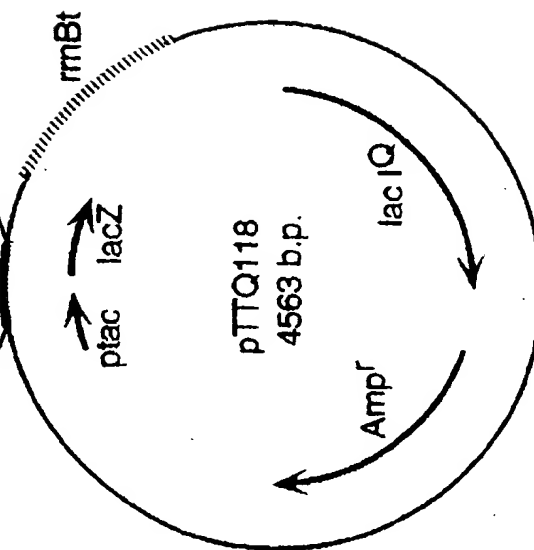


FIG. 14A

RBS: Ribosome binding site lacZ: Beta-galactosidase alpha fragment
 ptac: Synthetic tac promoter rmBt: E. coli rmB transcription terminator
 lac I^Q: Lac repressor gene

FIG. 14C

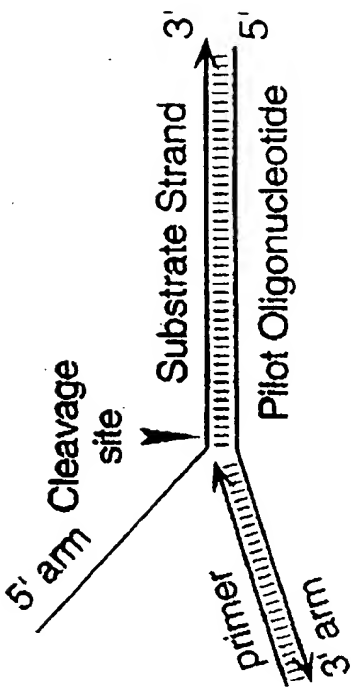


FIG. 16B

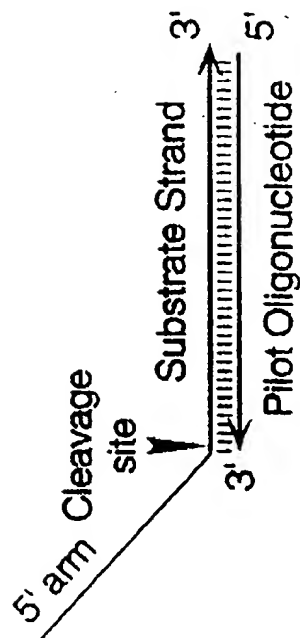


FIG. 16D

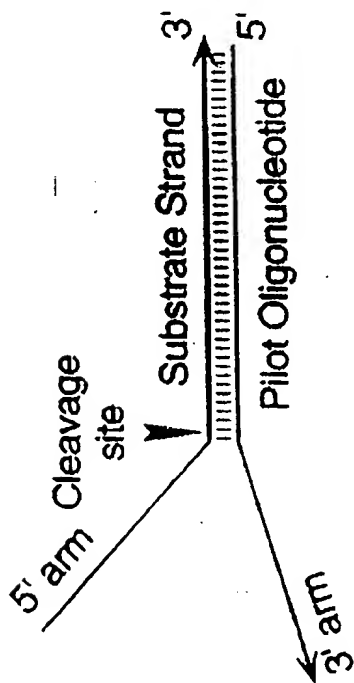


FIG. 16A

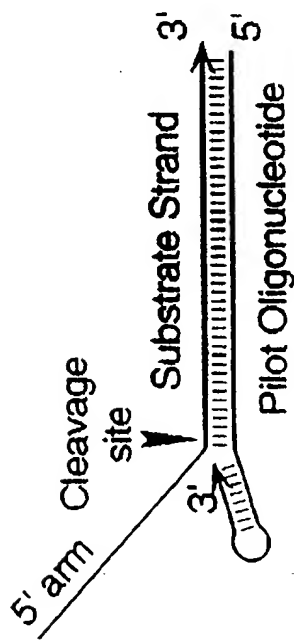


FIG. 16C

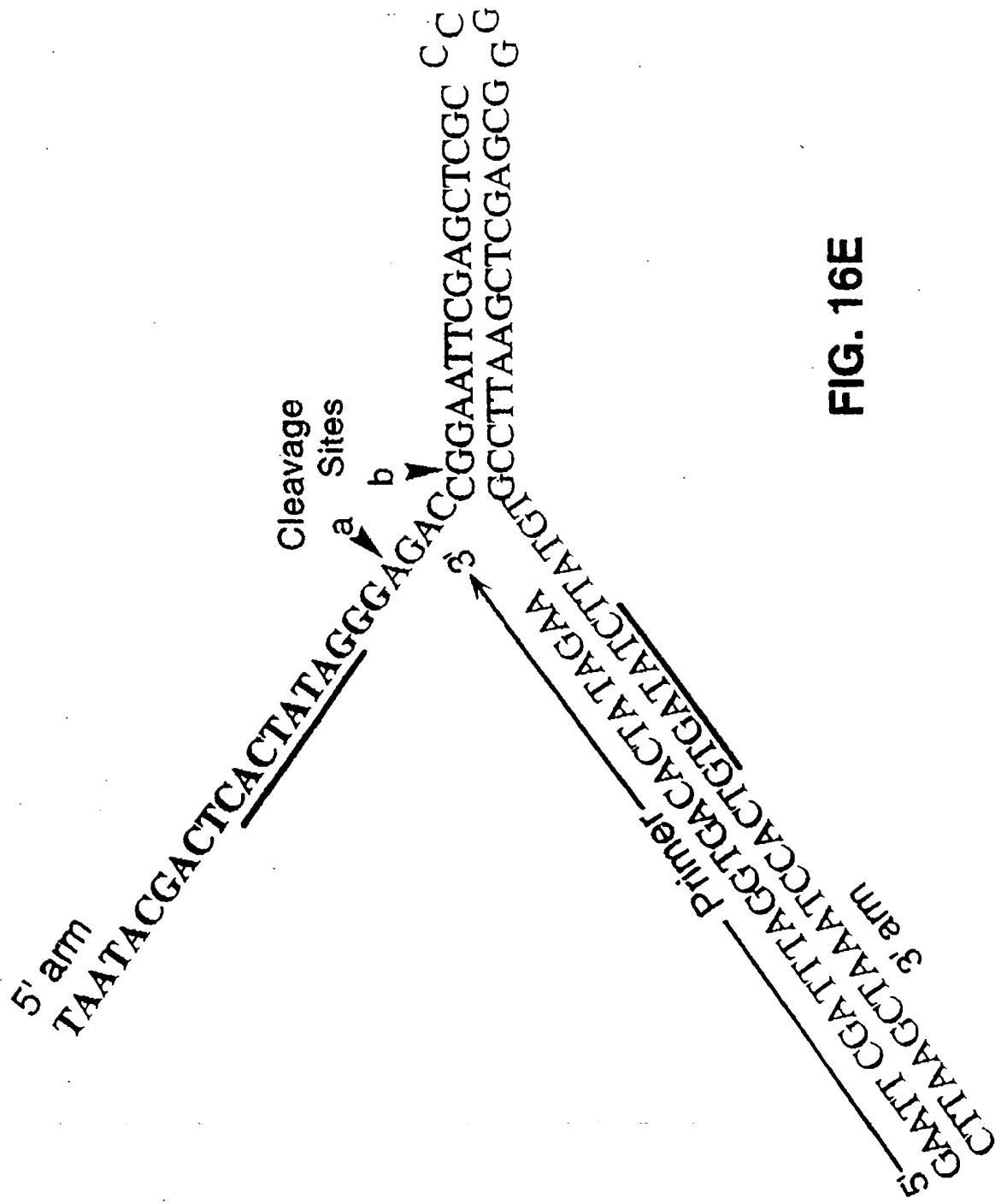
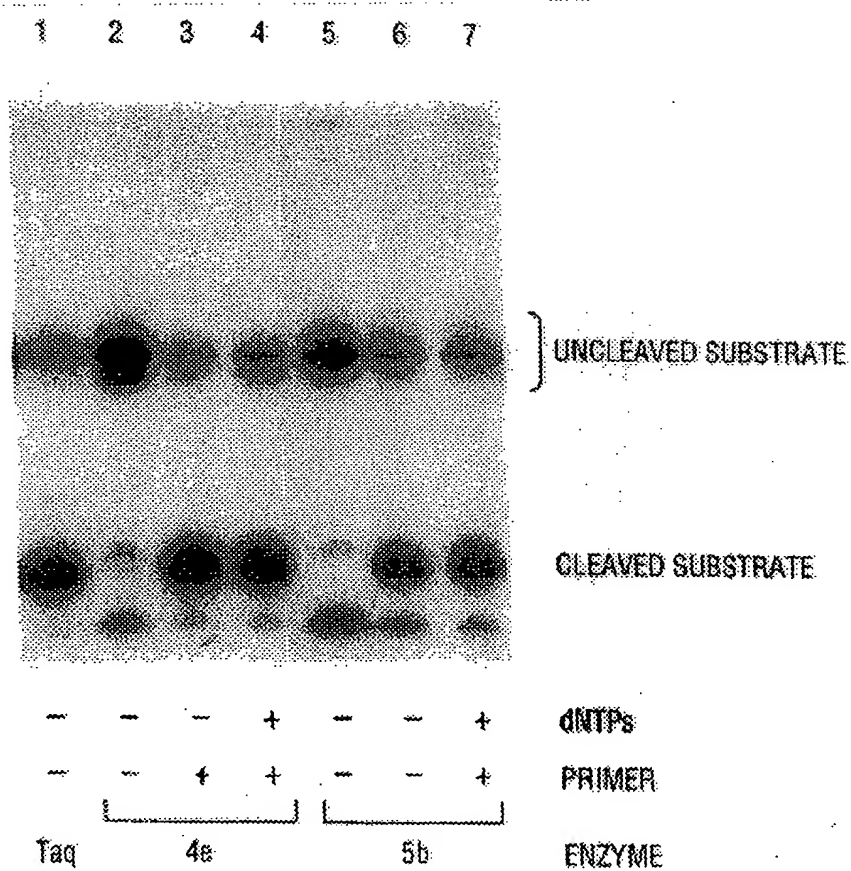


FIG. 16E

FIG. 17



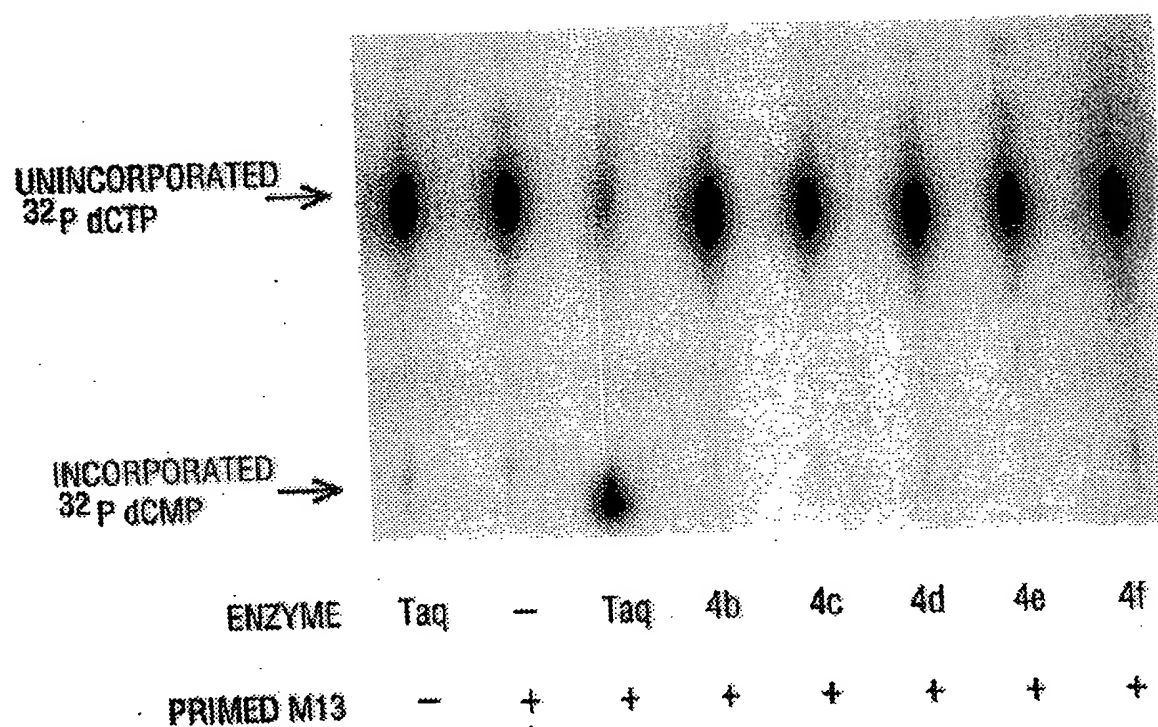


FIG. 18

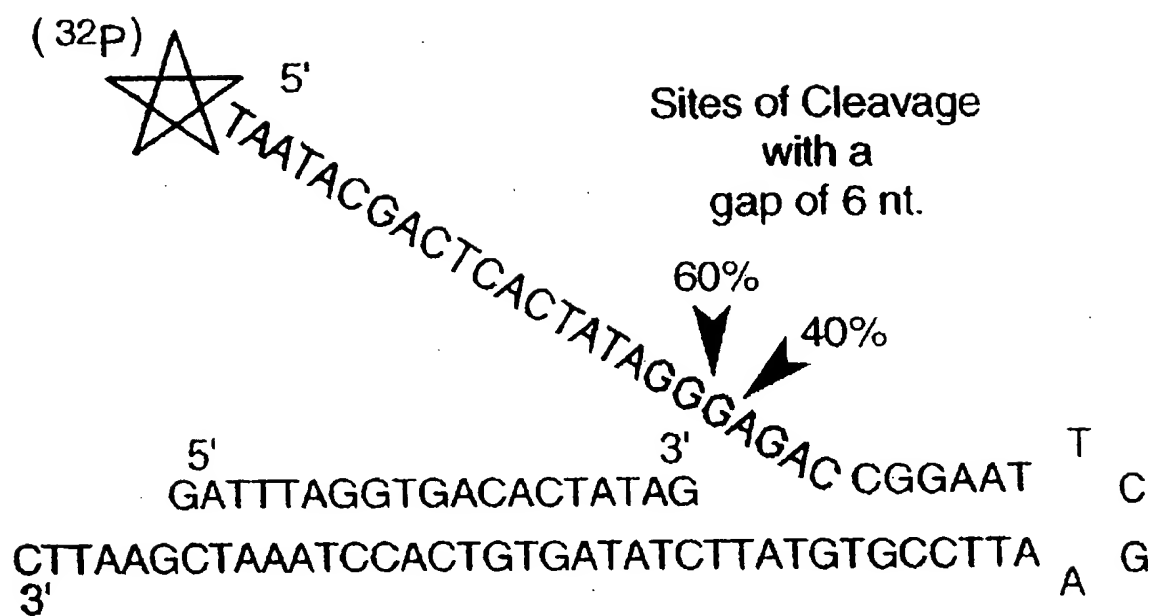


FIG. 19A

84 NUC. ———

HAIRPIN TEST MODULE

CONVERSION TO DOUBLE STRANDED
(COMPLETE EXTENSION OF PRIMER)

DESIRED PRODUCT 21 NUC. ———→

MULTIPLE BANDS
CAUSED BY POLYMERIZATION

FIG. 19B

SOME ABERRANT CLEAVAGE WITH '46'
BECAUSE OF RESIDUAL POLYMERASE ACTIVITY.

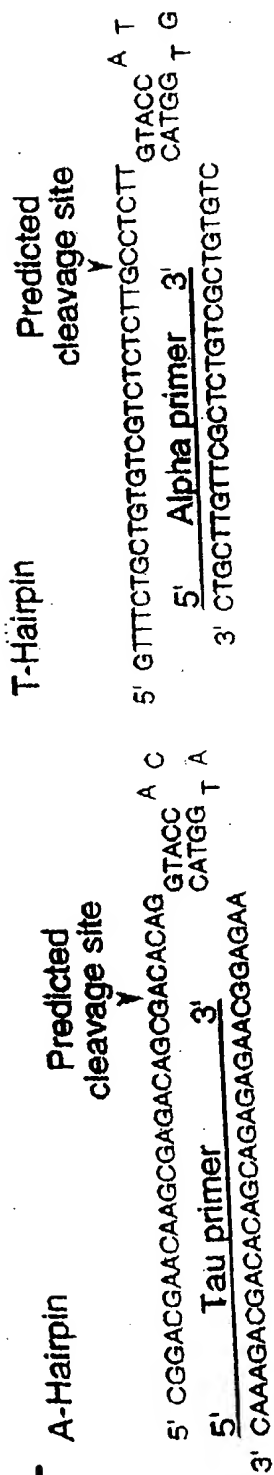


FIG. 20A

Sequence of alpha primer:

5' GACGAACAAGCGAGACAGCG 3'

FIG. 20B

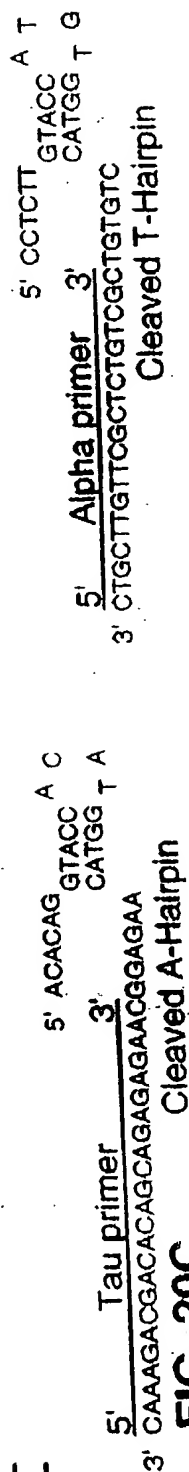


FIG. 20C

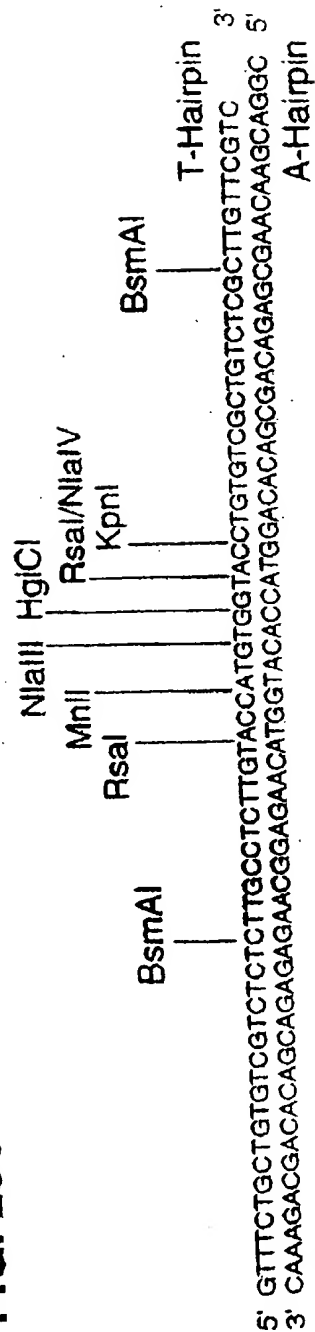


FIG. 20D

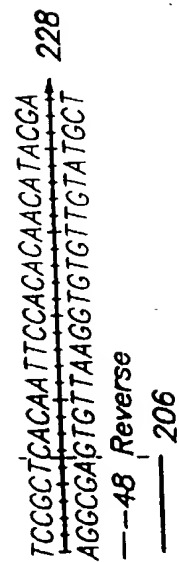
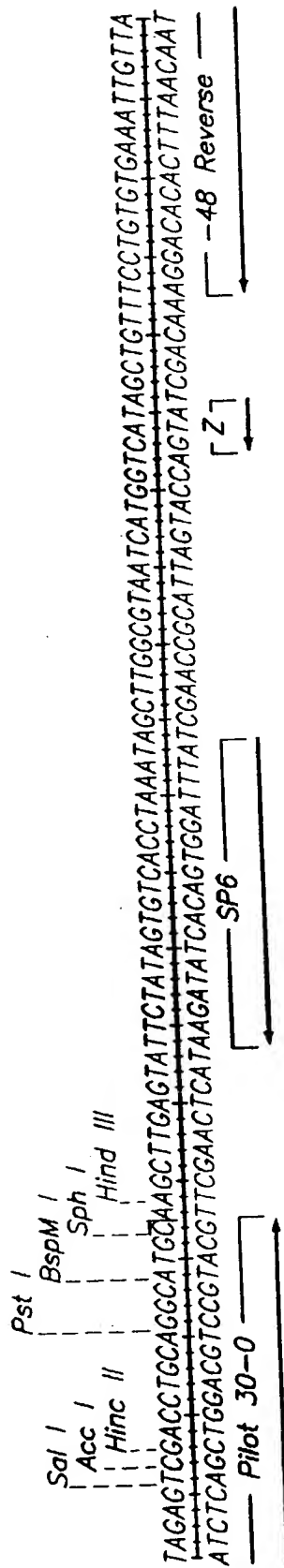
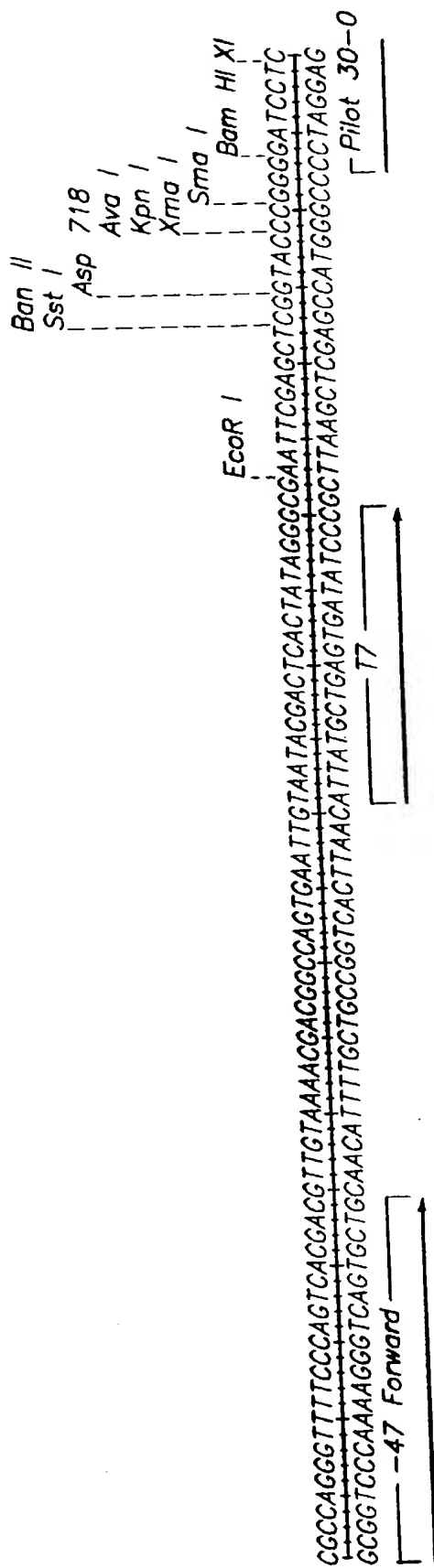


FIG. 21

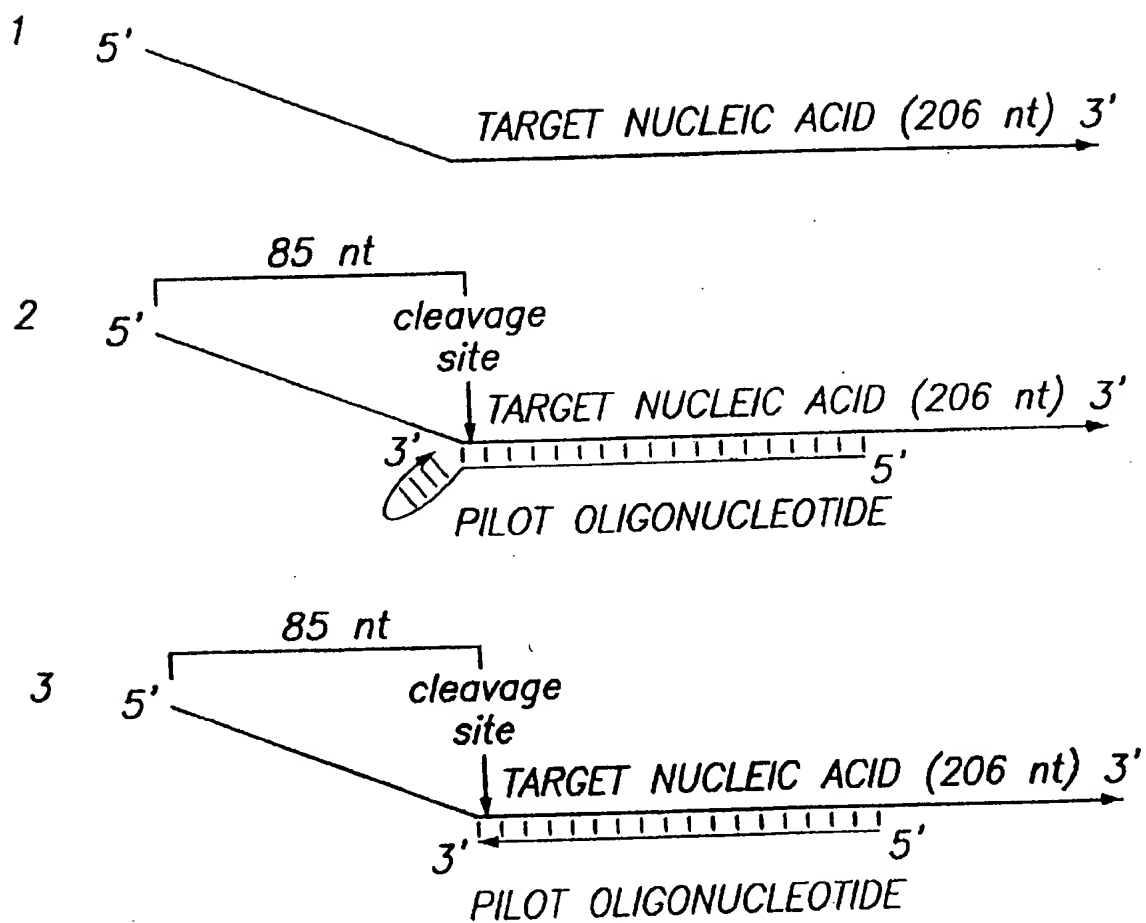


FIG. 22A

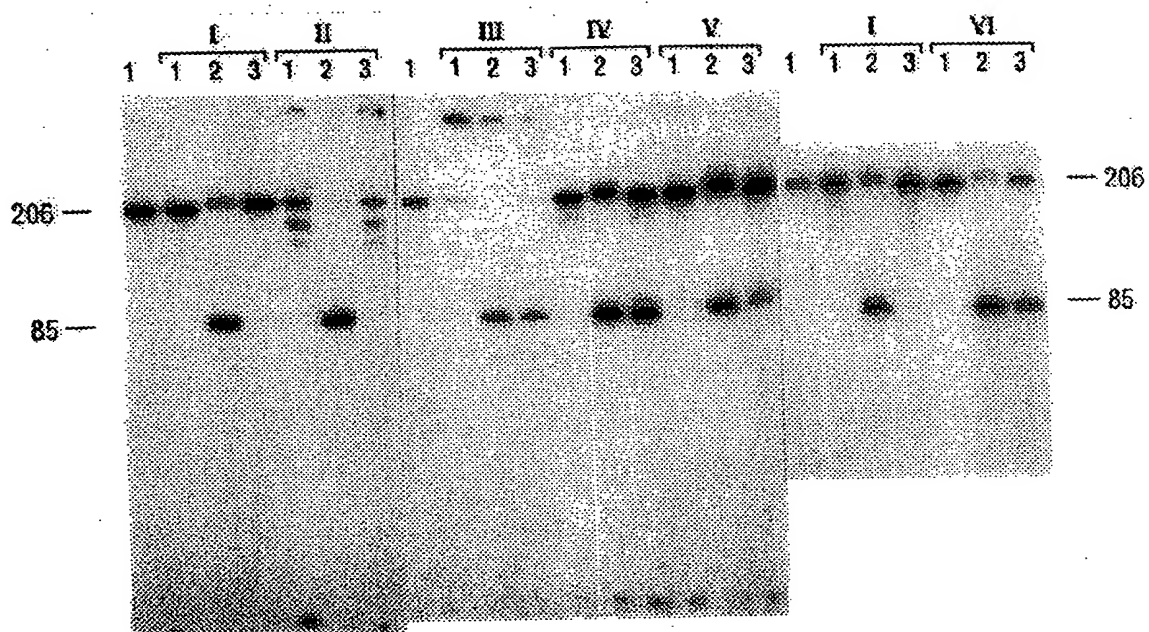


FIG. 22B

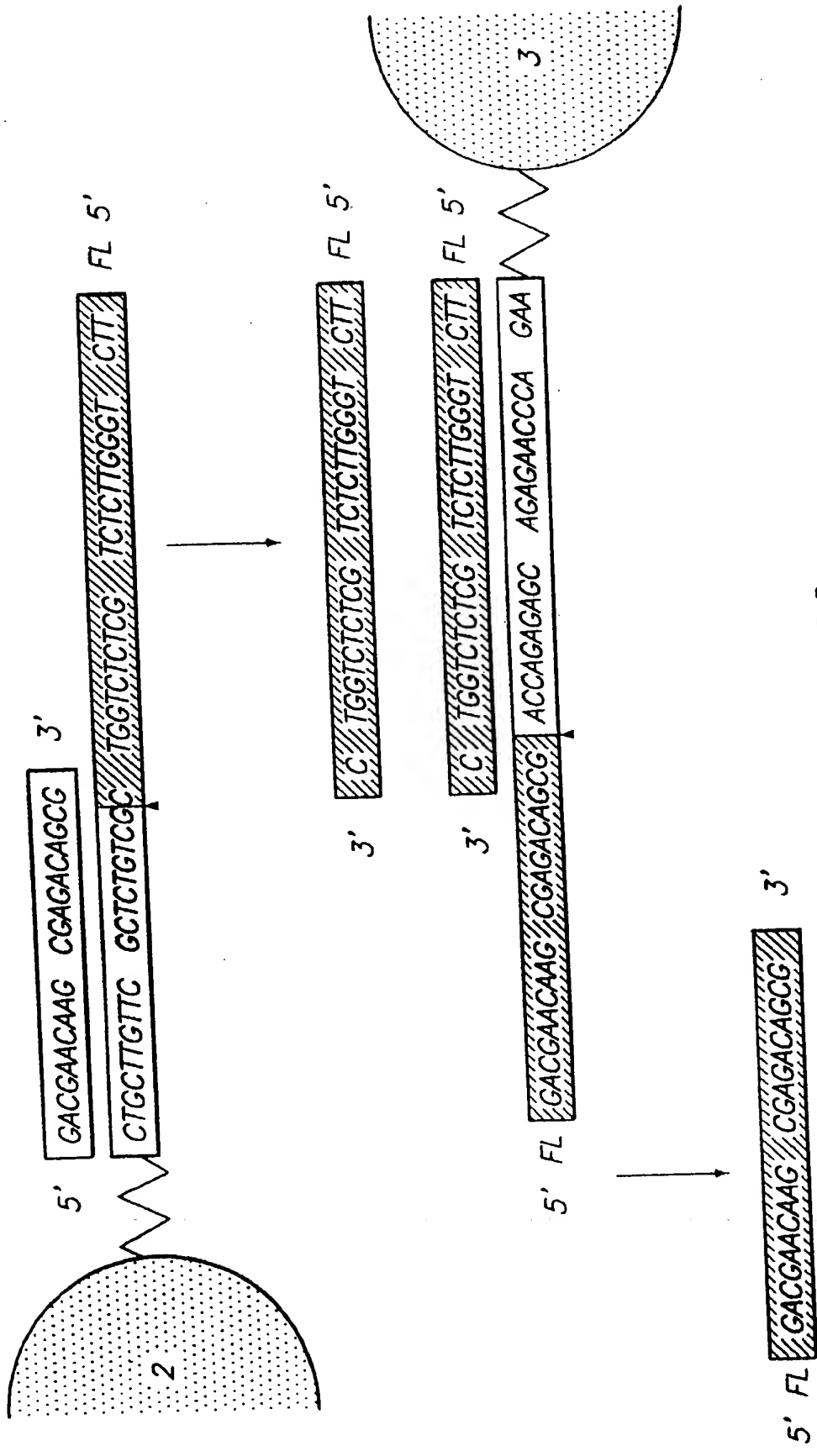


FIG. 23

CDR BEAD		T	T	T	AT	AT	A	A	A	
PILOT		-	-	+	-	+	+	-	-	
CLEAVASE	M	M	-	+	+	+	+	+	-	M

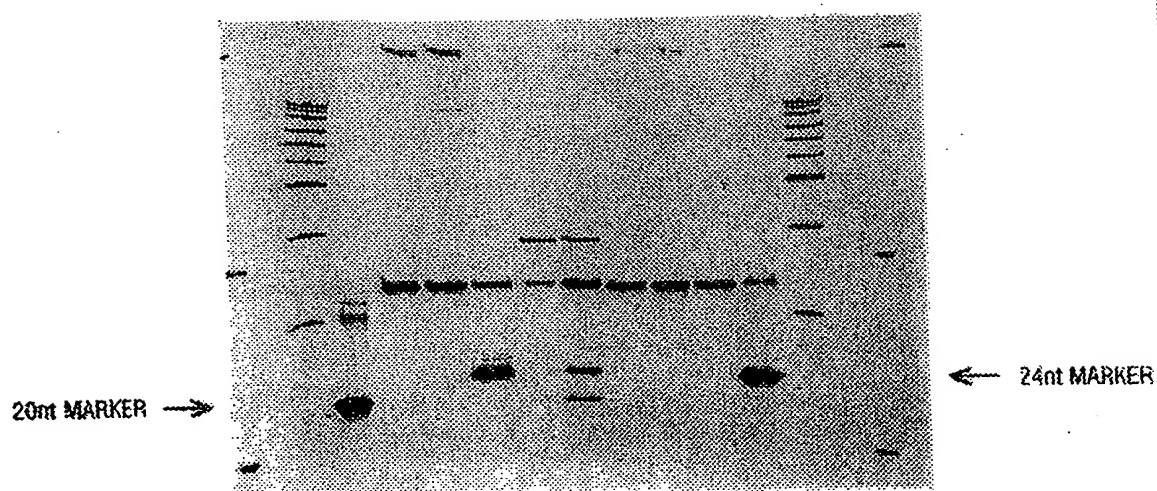


FIG. 24

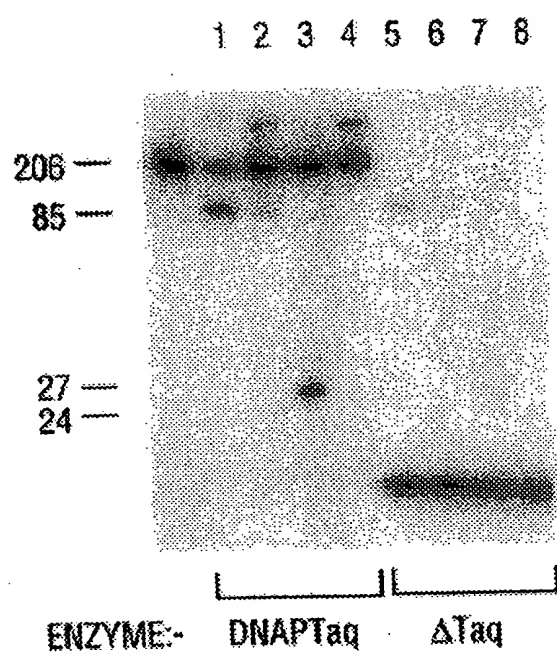


FIG. 25A

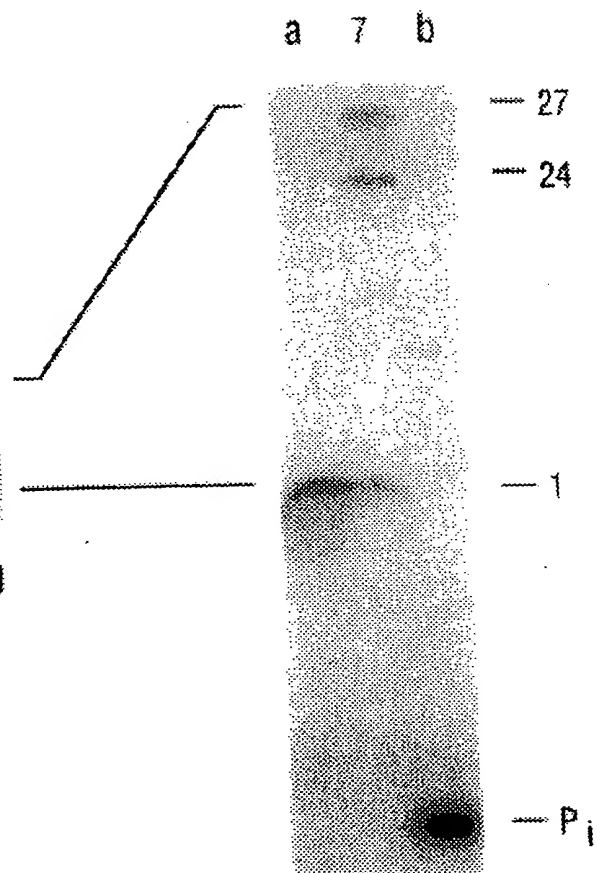


FIG. 25B

FIG. 26A

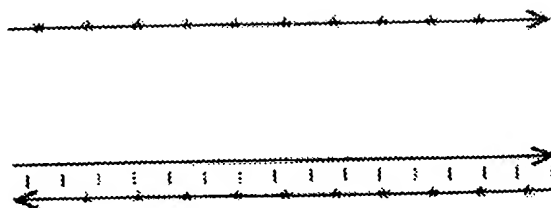
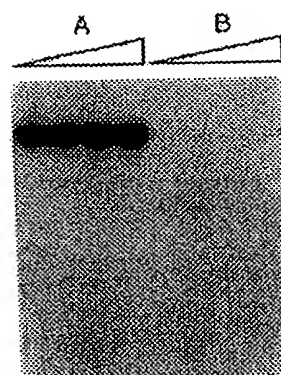


FIG. 26B

* = 32p



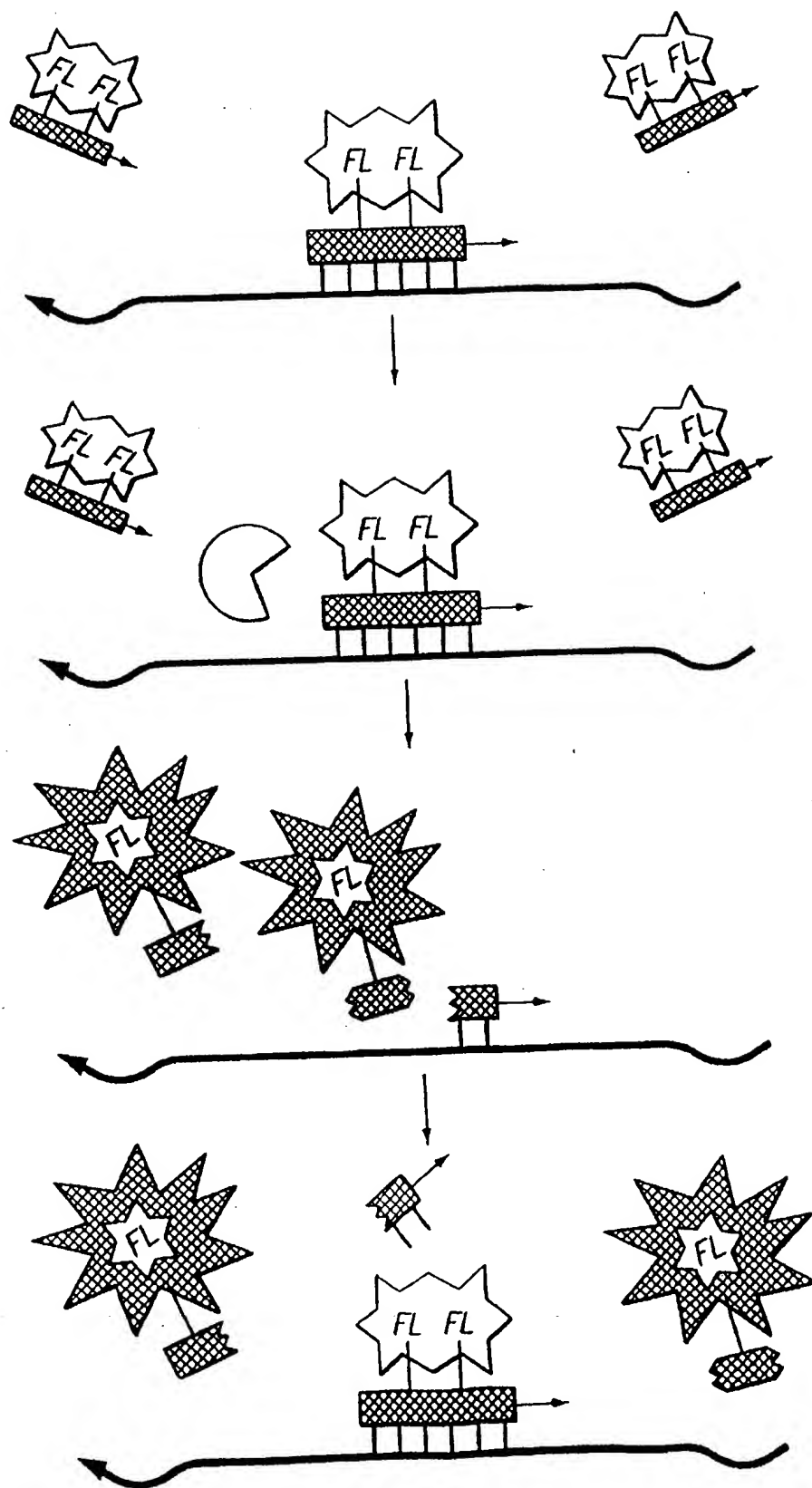


FIG. 27

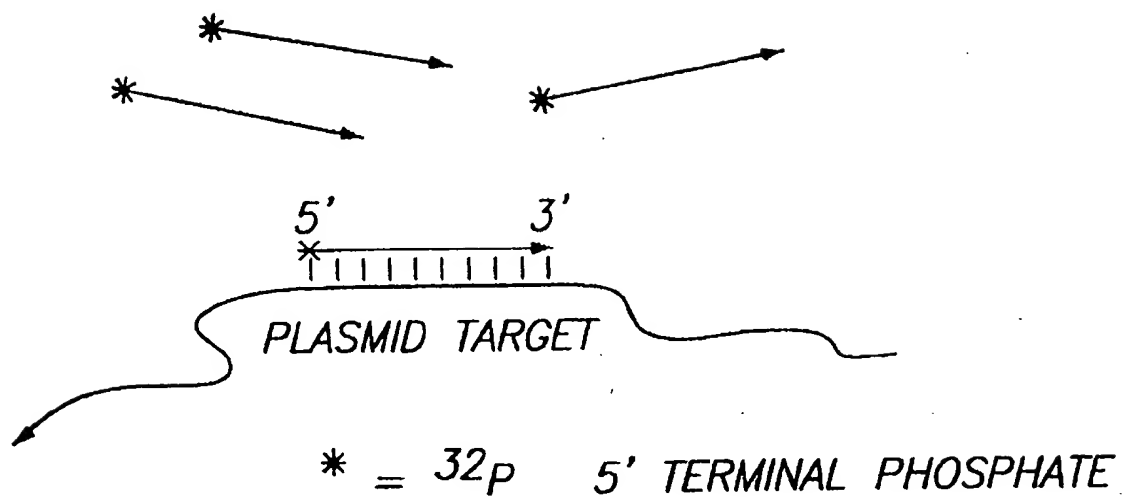


FIG. 28A

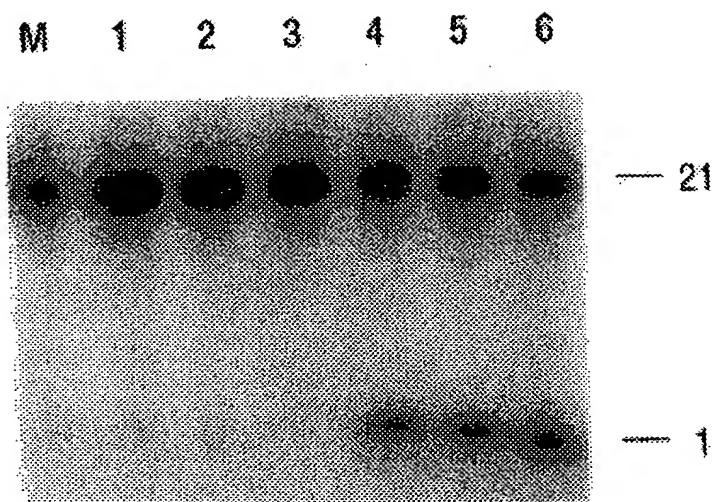


FIG. 28B

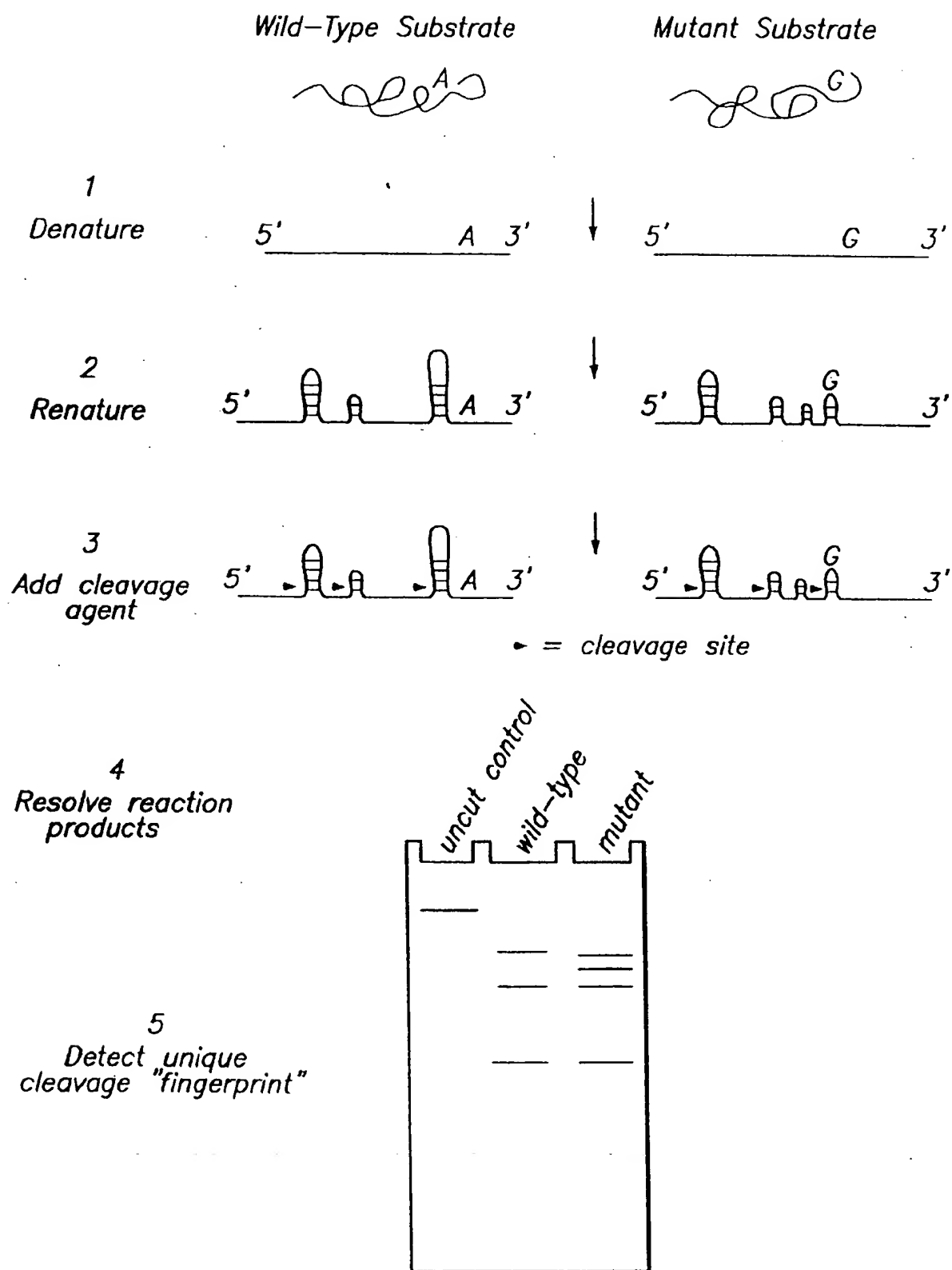


FIG. 29

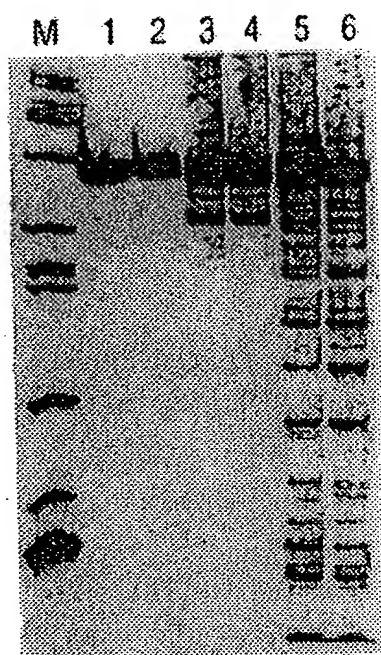


FIG. 30

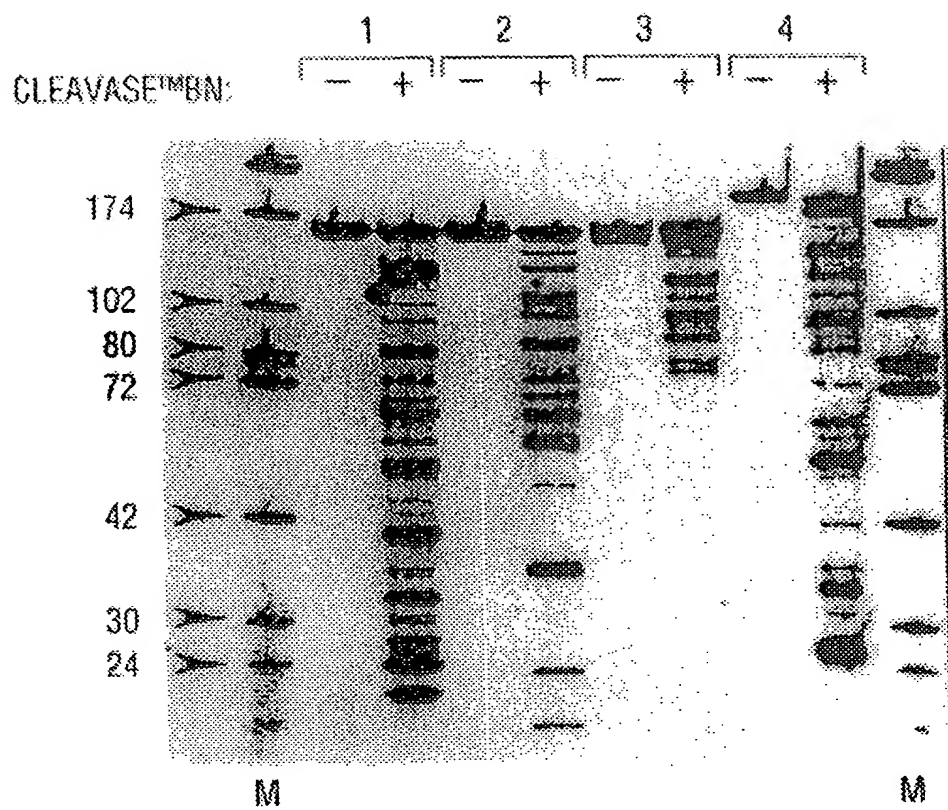


FIG. 31

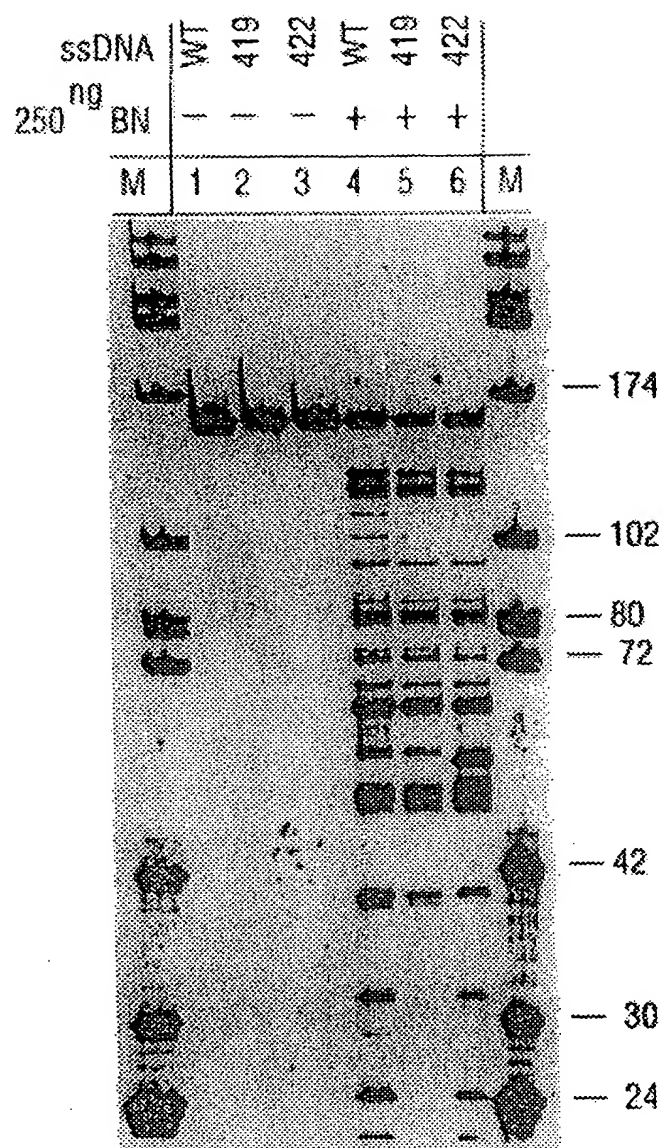
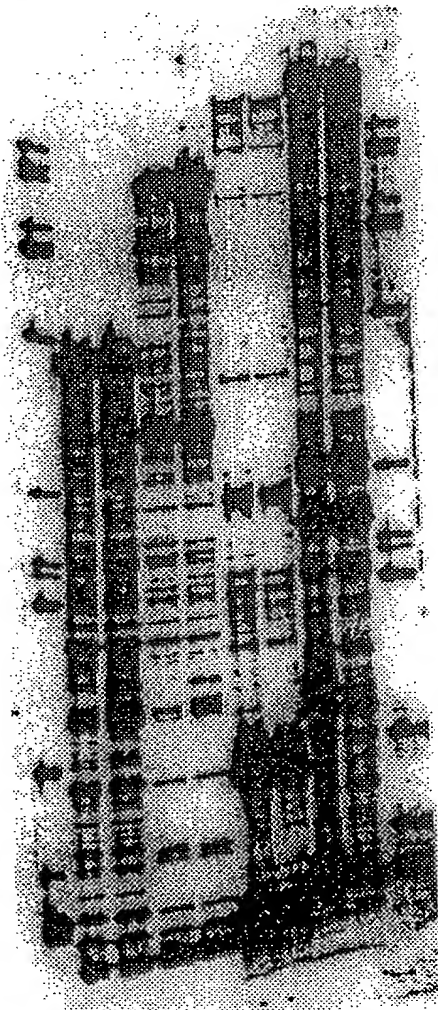


FIG. 32

157 378 1056 1587
M 1 2 3 4 5 6 7 8 M



WT 422 WT 422 WT 422 WT 422

FIG. 33

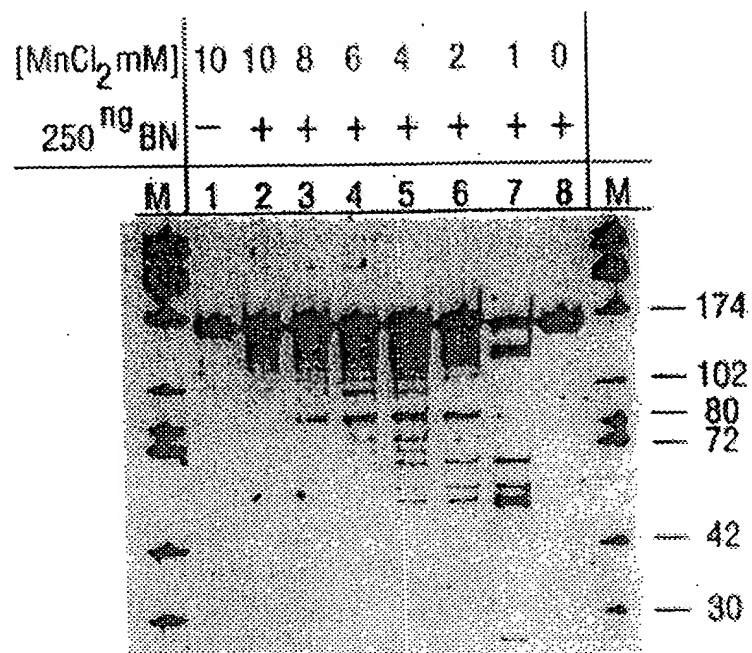


FIG. 34

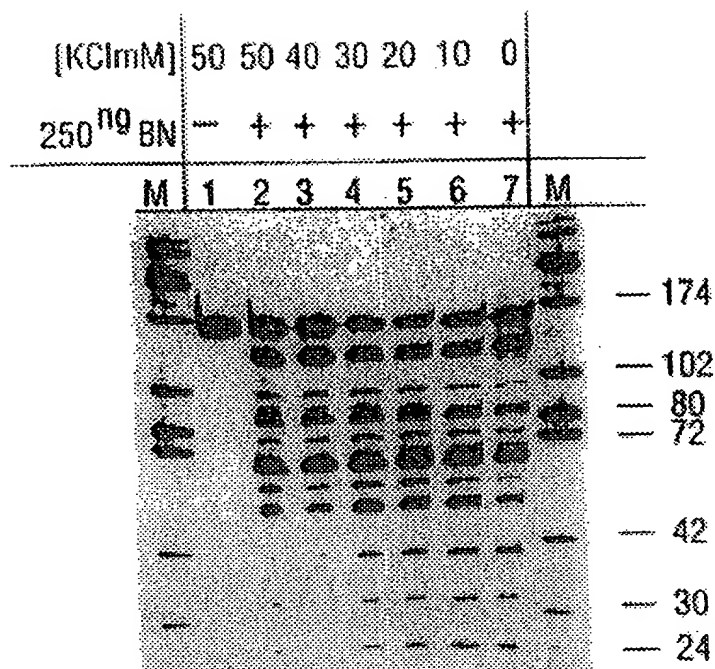


FIG. 35

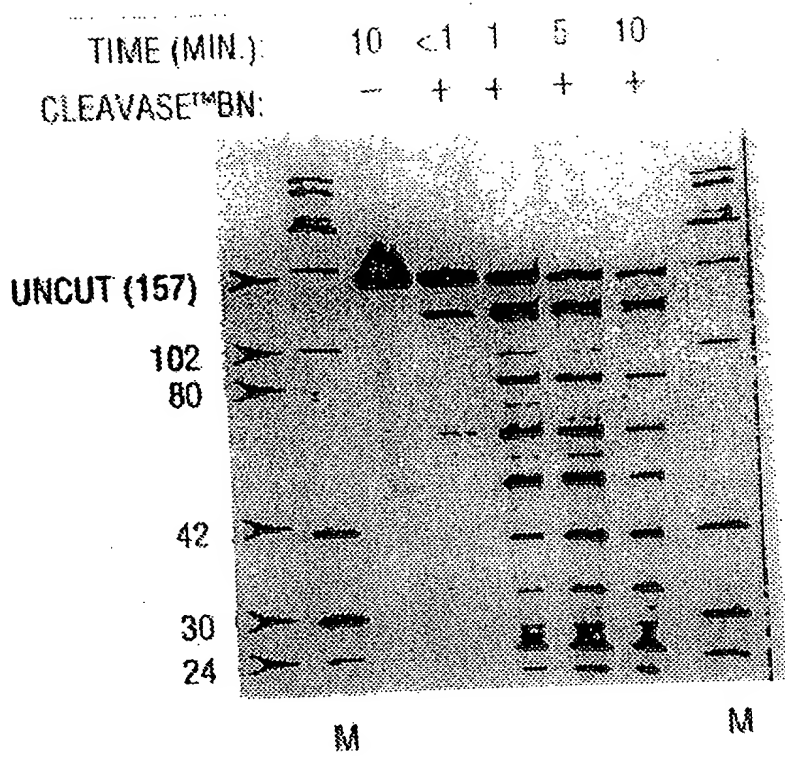


FIG. 36

TEMPERATURE (°C):	55	80	55	60	65	70	75	80
CLEAVASE TM BN:	-	-	+	+	+	+	-	+

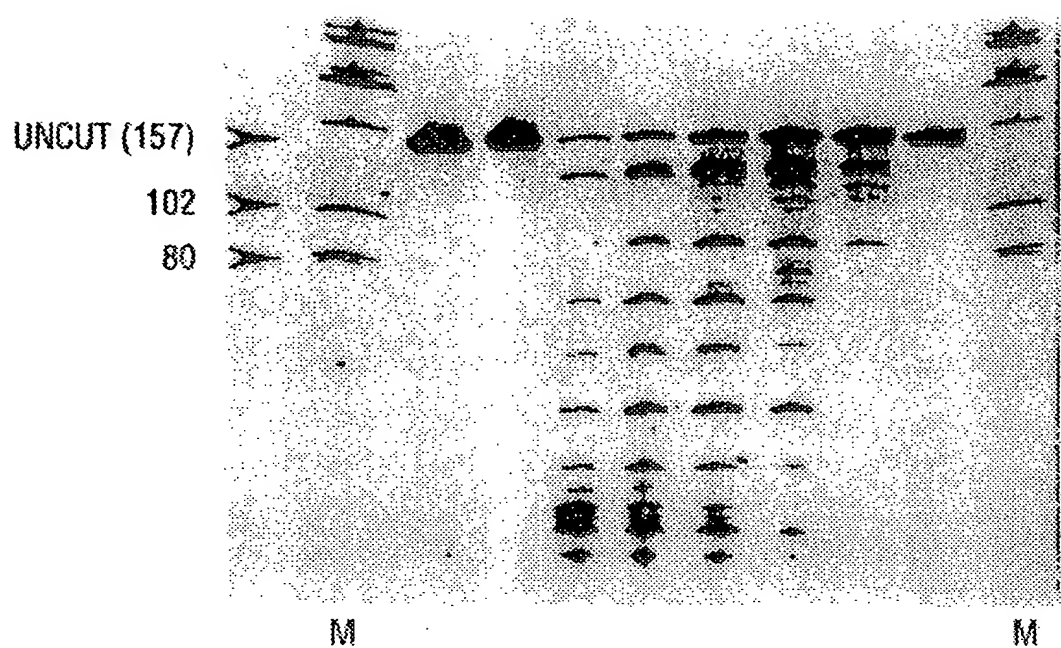


FIG. 37

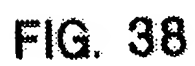


FIG. 38

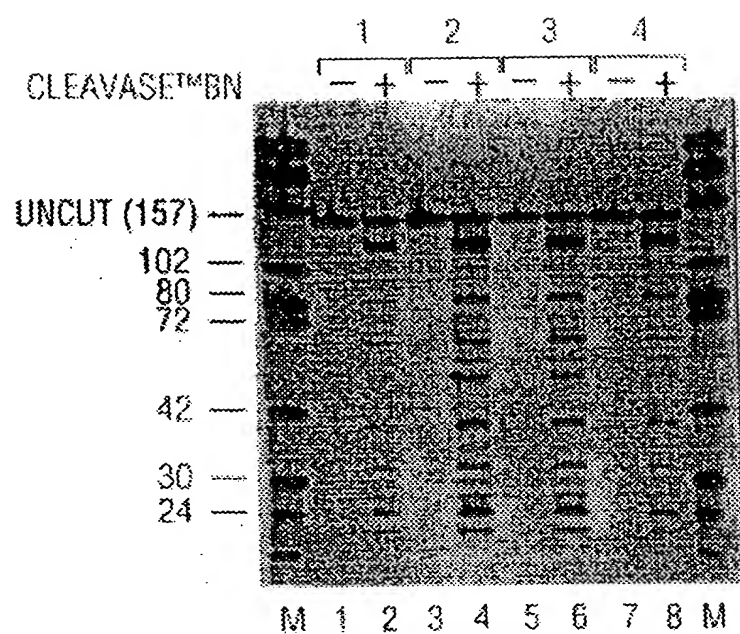


FIG. 39

STRAND	5' - BIOTIN SENSE STRAND						5' - FLUORESCCEIN ANTI-SENSE STRAND					
	WT	419	422	WT	419	422	WT	419	422	WT	419	422
ssDNA	WT	419	422	WT	419	422	WT	419	422	WT	419	422
250 ^{ng} BN	-	-	-	+	+	+	+	+	+	-	-	-
M	1	2	3	4	5	6	7	8	9	10	11	12

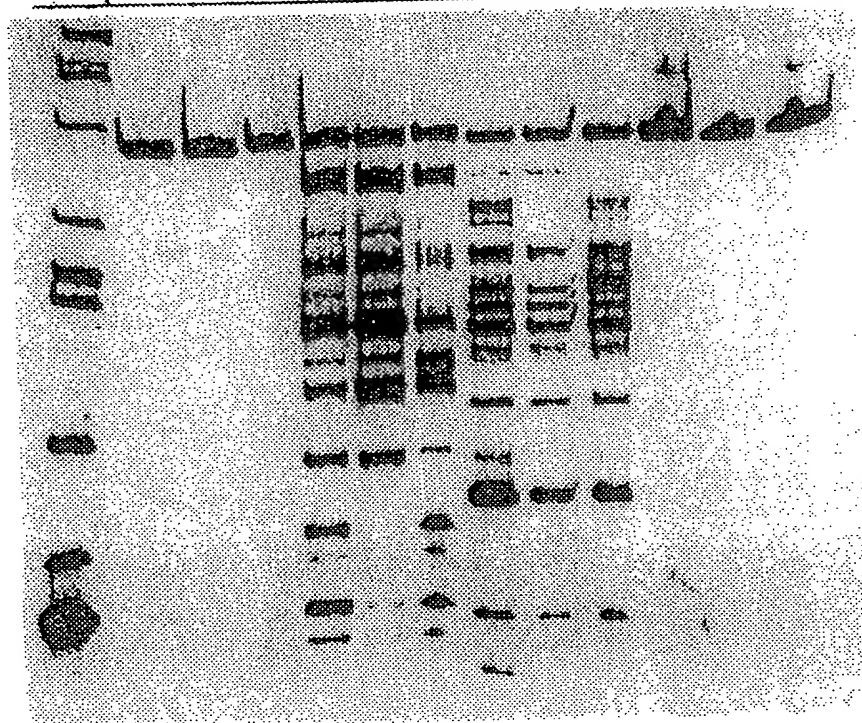


FIG. 40

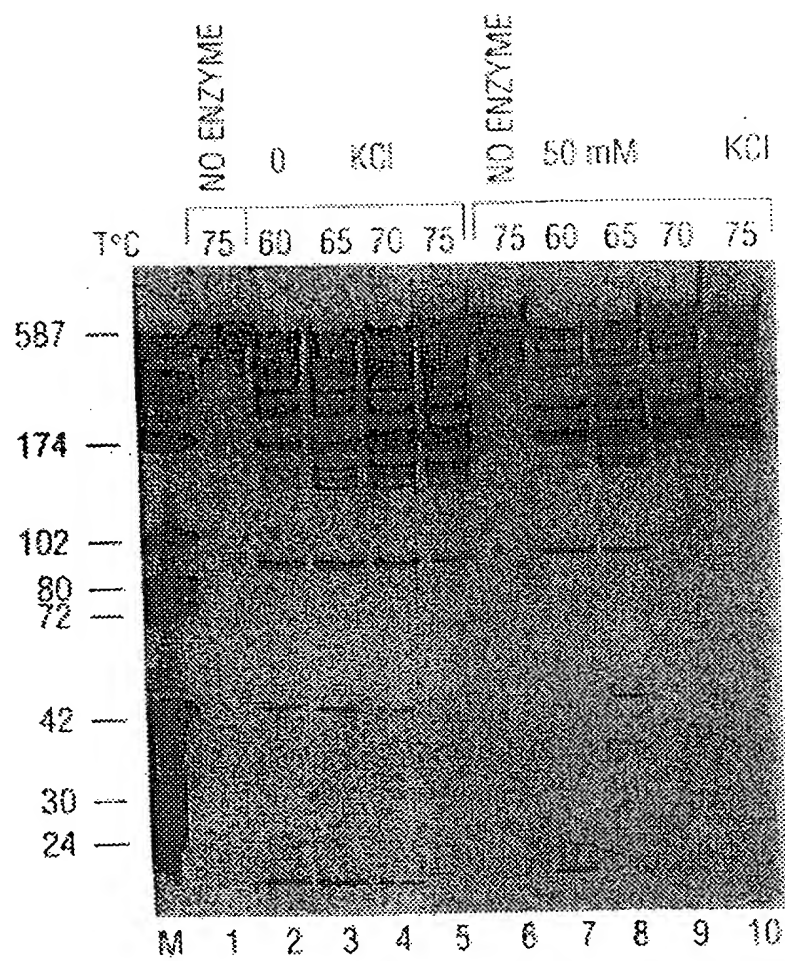


FIG. 41

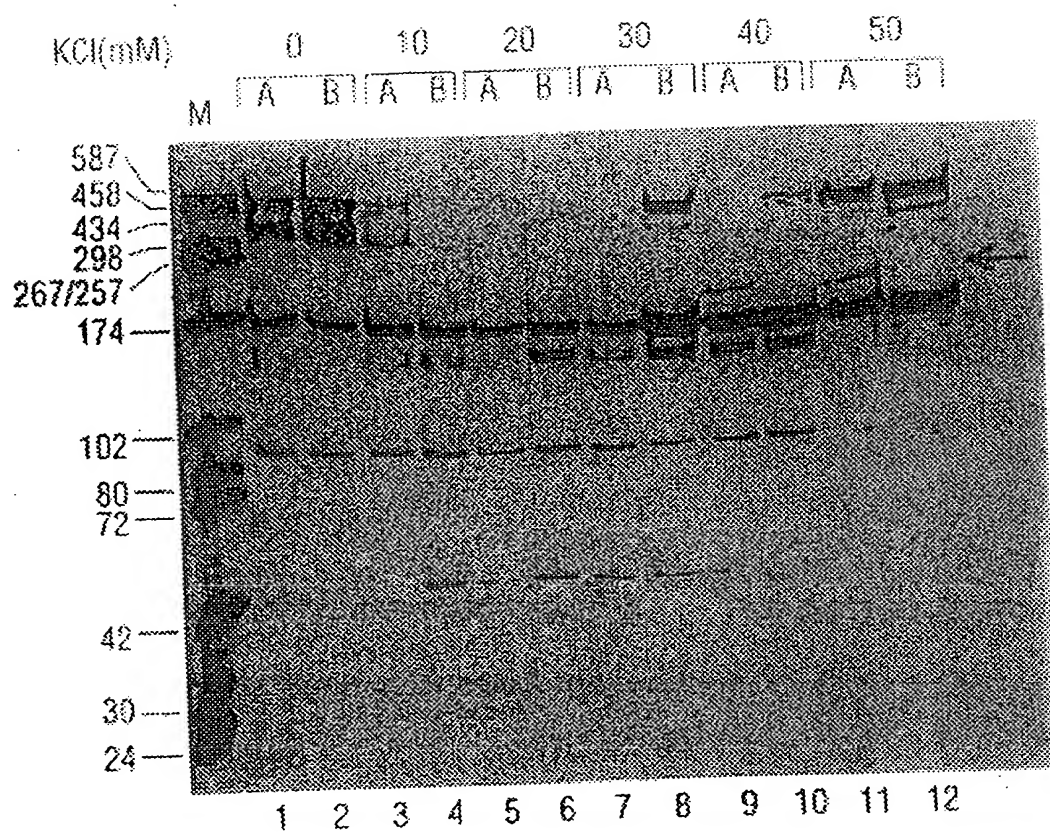


FIG. 42

CLEAVASE™BN

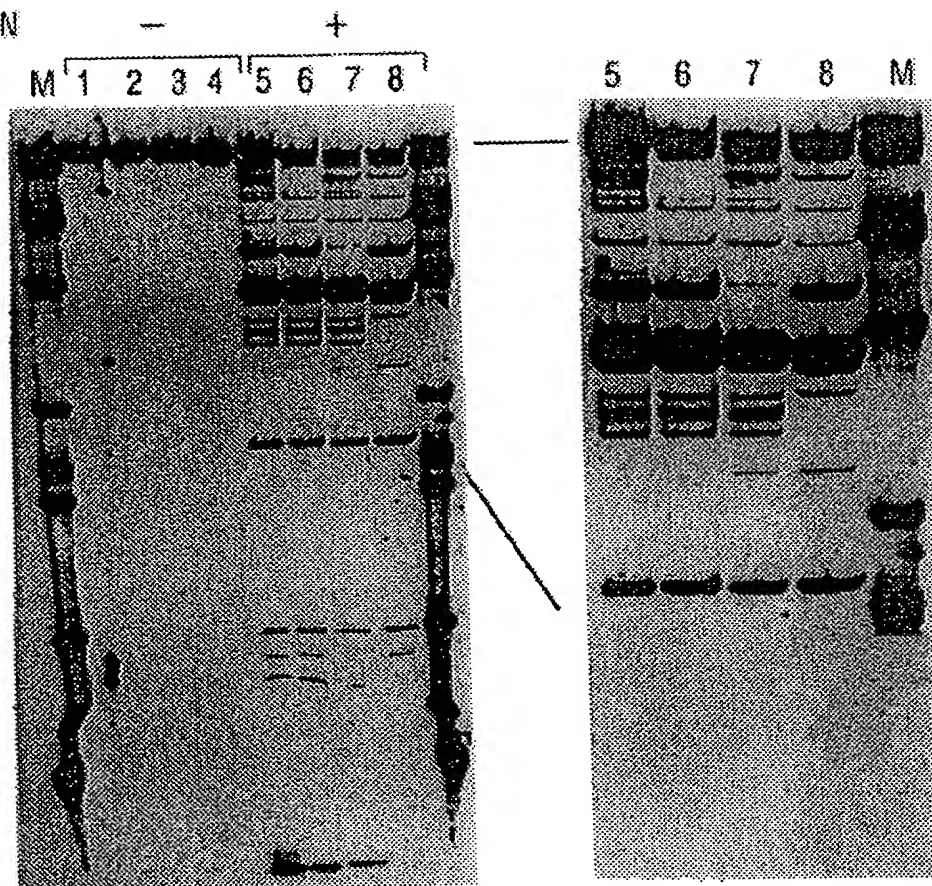


FIG. 43

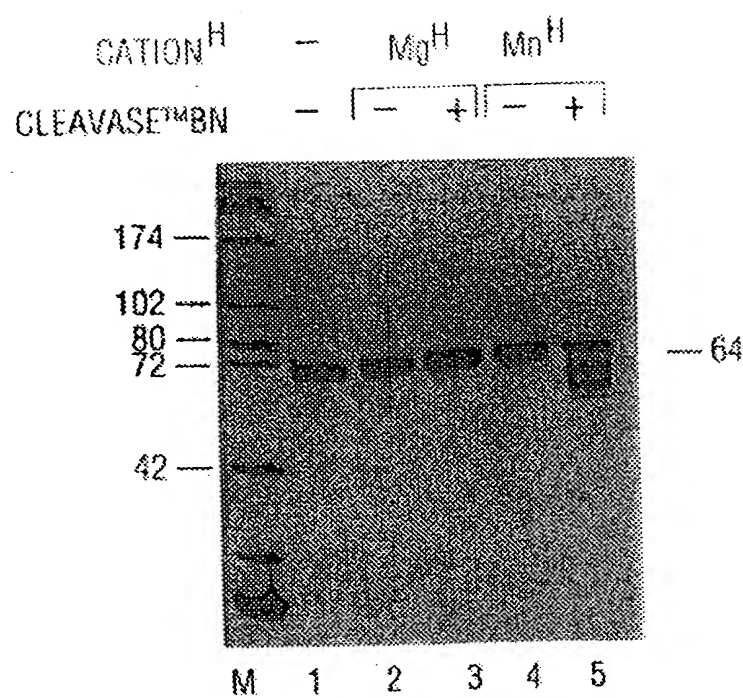


FIG. 44

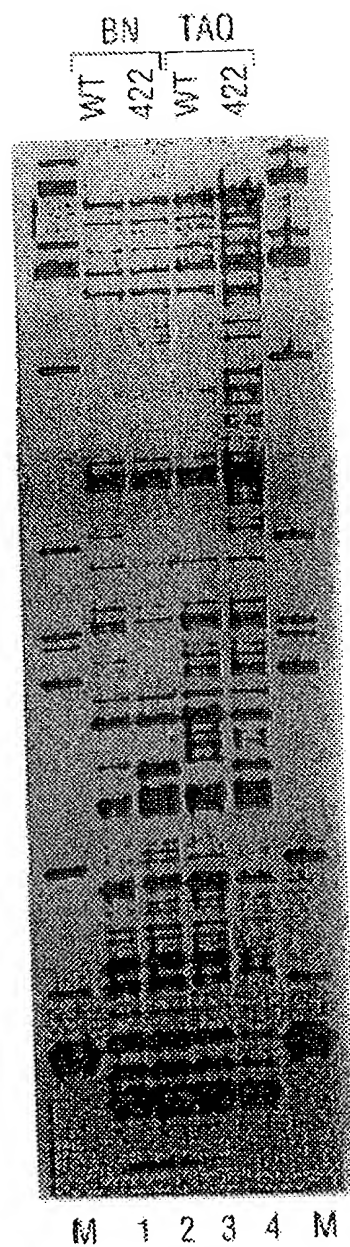


FIG. 45

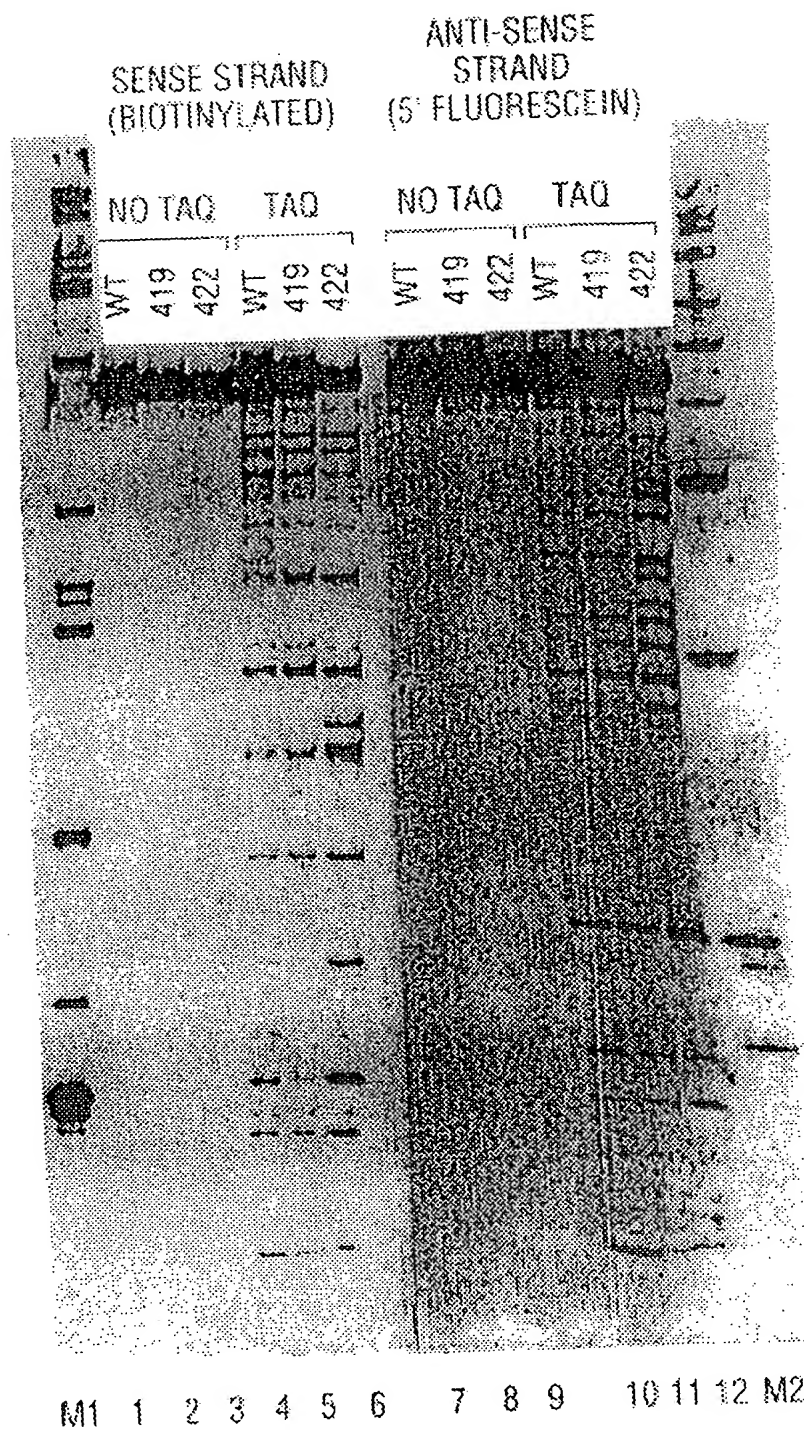


FIG. 46

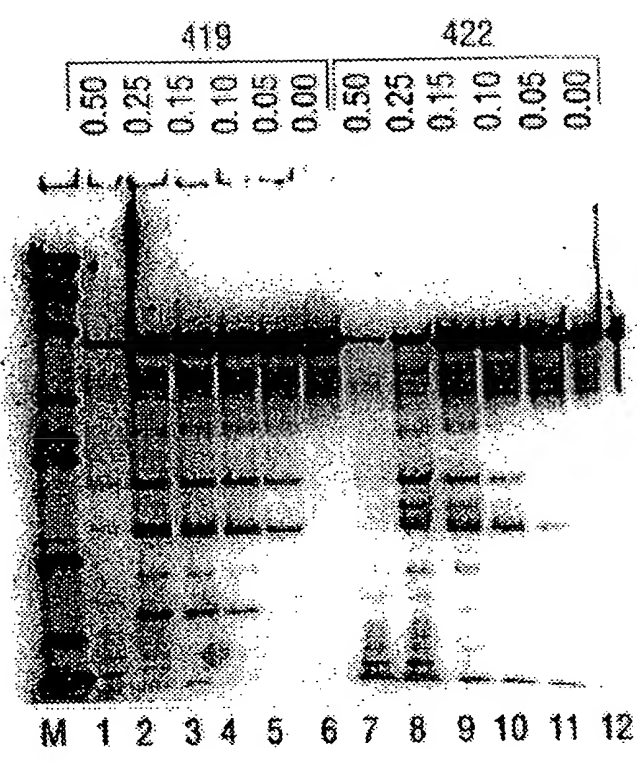


FIG. 47

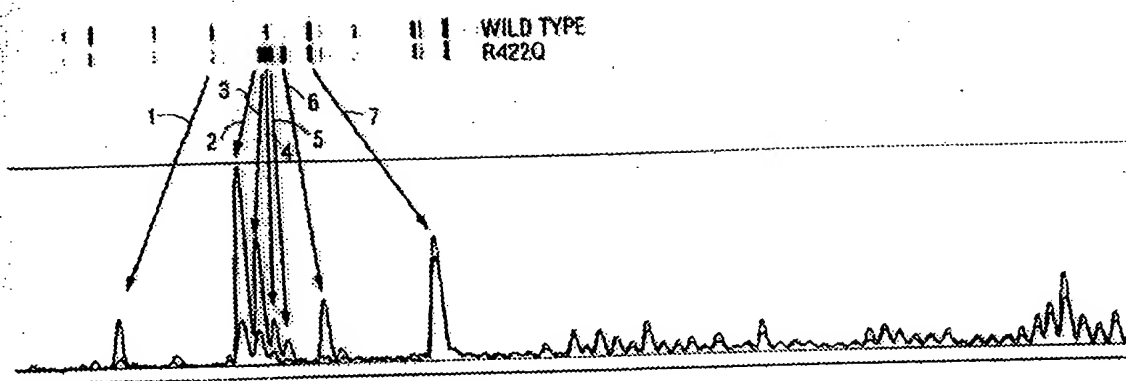


FIG. 48

L.100.8-1
(SEQ ID NO: 76) 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

L.46.16-10
(SEQ ID NO: 77) 5'GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCTTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L.46.16-12
(SEQ ID NO: 78) 5'GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCTTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L19.16-3
(SEQ ID NO: 79) 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

L.CEM/251
(SEQ ID NO: 80) 5'GGCTGACAAGAAGGAAACTCGCTGAAACAGCAGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCTTTGAGCGACTTTGTGTCGTCCCTGAAAGGTGTTCCCC

L.36.8-3
(SEQ ID NO: 81) 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

FIG. 49A

L.100.8-1 (SEQ ID NO: 76)	<div>100</div> <p>ATGTTACGGGGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT TACAATGCCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGTGAGAGA</p>
L.46.16-10 (SEQ ID NO: 77)	<p>ATGTTATGGGGAGG-----AGCCGGTCGGGAACACCCACTTTCT TACAATACCCCTCC-----TCGGCCAGCCCTTGTTGGGTGAAAGA</p>
L.46.16-12 (SEQ ID NO: 78)	<p>ATGTTATGGGGAGG-----AGCCGGTCGGGAACACCCACTTTCT TACAATACCCCTCC-----TCGGCCAGCCCTTGTTGGGTGAAAGA</p>
L19.16-3 (SEQ ID NO: 19)	<p>ATGTTACGGGGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT TACAATGCCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGGGAGAGA</p>
L.CEM/251 (SEQ ID NO: 80)	<p>ATGTTACGGGGAGGTACTGGGAAGGAGCCGGTCGGGAACGCCCACTTTCT TACAATGCCCCCTCCATGACCCCTTCTCGGCCAGCCCTTGCGGGTGAAAGA</p>
L.36.8-3 (SEQ ID NO: 81)	<p>ATGTTACGGGAGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT TACAATGCCCTCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGTGAGAGA</p>

FIG. 49B

L.100.8-1

5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTCAGTCGCTCTGCGGA
3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT

L.46.16-10

5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTCAGTCGCTCTGCGGA
3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT

L.46.16-12

5'TGGTGTATAAATATCACTGCATTTTCGCTCTGTATTCAGTCGCTCTGCGGA
3'ACCACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT

L.19.16-3

5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTCAGTCGCTCTGCGGA
3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT

L.CEM/251

5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTCAGTCGCTCTGCGGA
3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT

L.36.8-3

5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTCAGTCGCTCTGCGGA
3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT

FIG. 49C

200

L.100.8-1

GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTTAG
CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC

L.46.16-10

GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTTAG
CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC

L.46.16-12

GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTTAG
CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC

L.19.16-3

GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTTAG
CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC

L.CEM/251

GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTTAG
CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC

L.36.8-3

GAGGCTGGCAGATTGAGCCCTAGGAGGTTCTCTCCAGCACTAGCAGGTTAG
CTCCGACCGTCTAACTCGGGATCCTCCAAGAGAGGTCGTGATCGTCCATC

FIG. 49D

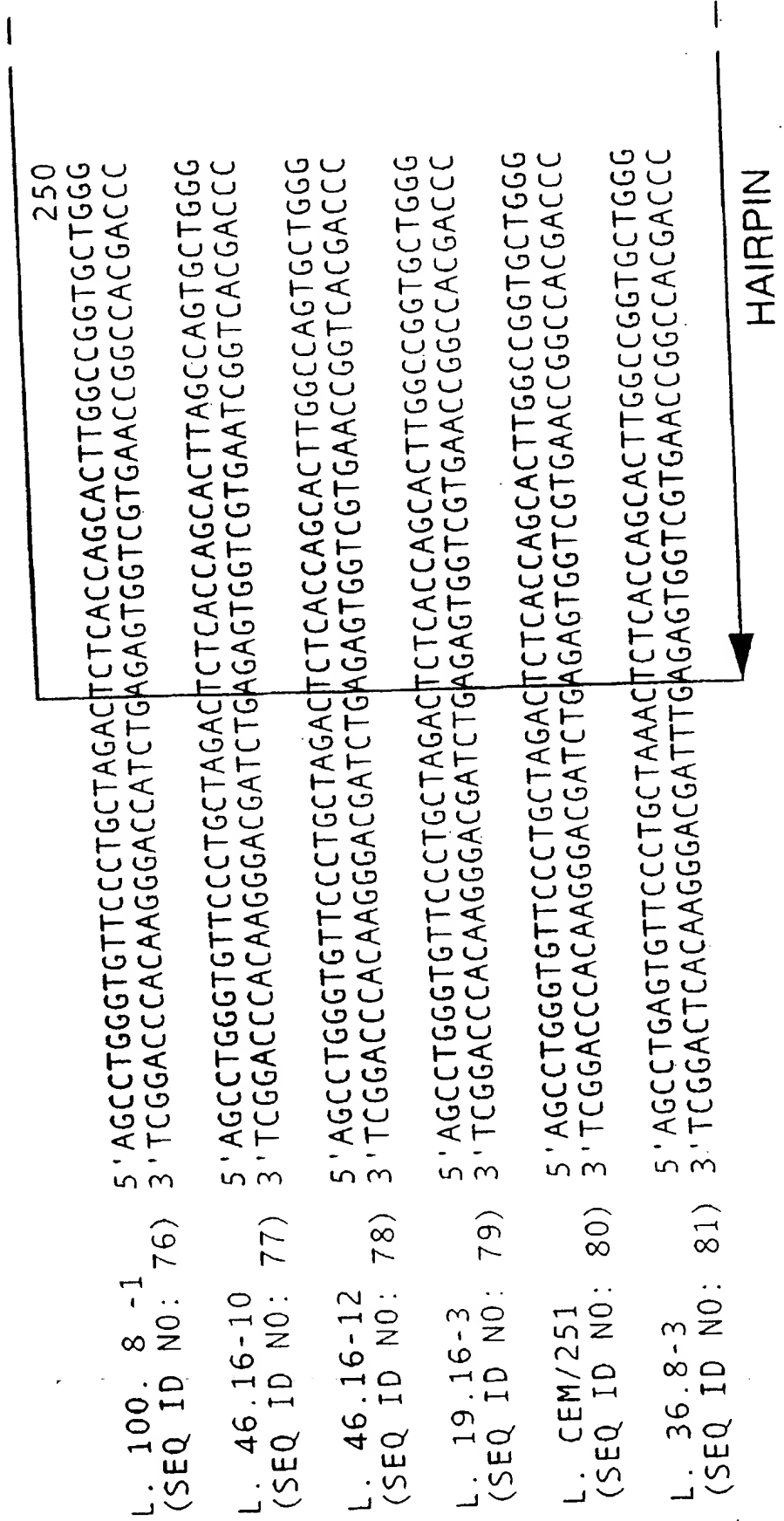


FIG. 49E

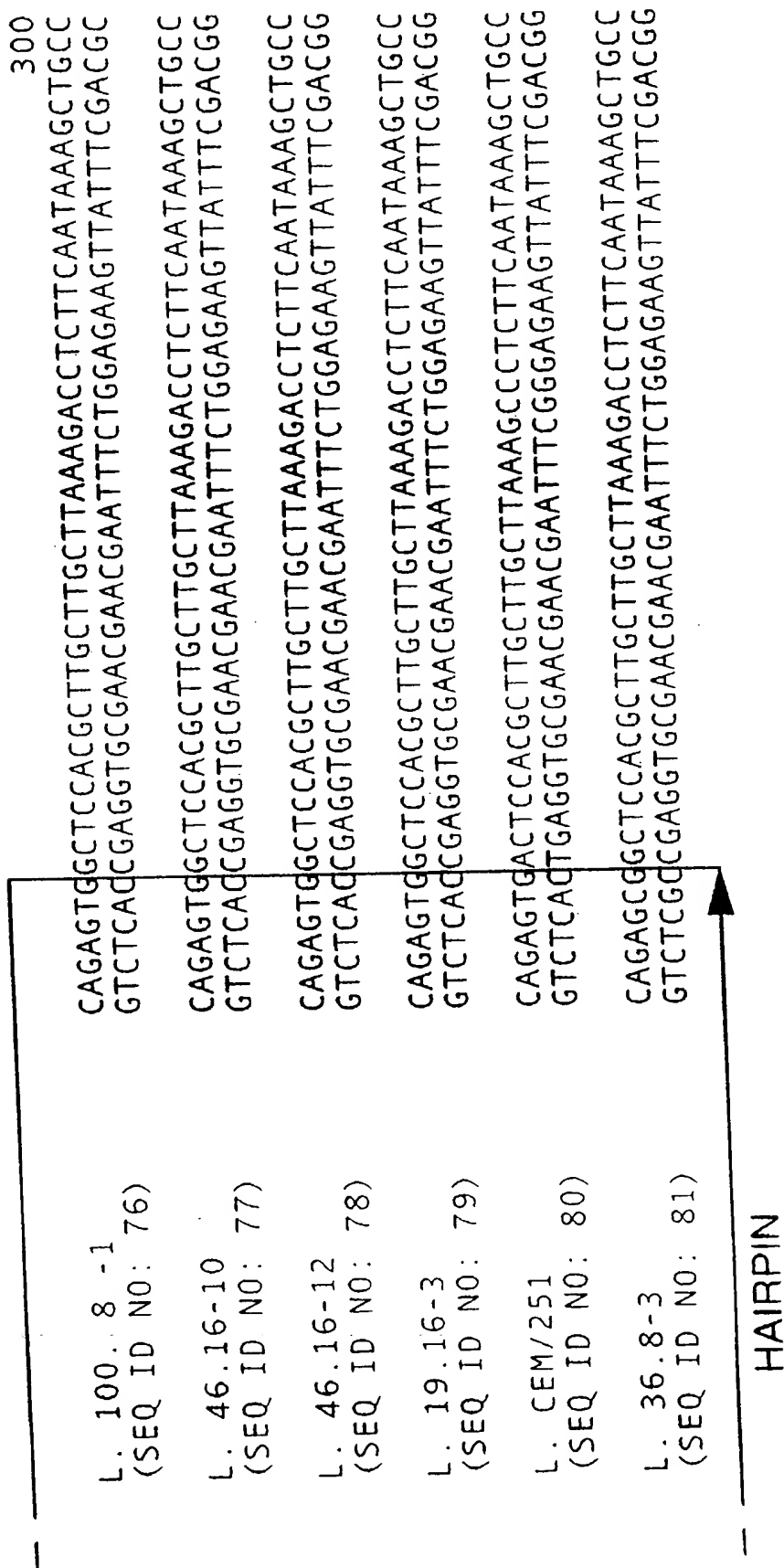


FIG. 49F

L. 100.8-1	<div>350</div> 5' ATTTT TAGAAGTAGGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3' 3' TAAATCTTCATCCGGTCACACACAAGGTTAGAGGATCGGCGCGGAC C 5'
L. 46.16-10	5' ATTTT TAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3' 3' TAAATCTTCATTCGGTCACACACAAGGTTAGAGGATCGGCGCGGAC C 5'
L. 46.16-12	5' ATTTT TAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3' 3' TAAATCTTCATTCGGTCACACACAAGGTTAGAGGATCGGCGCGGAC C 5'
L. 19.16-3	5' ATTTT TAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3' 3' TAAATCTTCATCCGATCACACACAAGGTTAGAGGATCGGCGCGGAC C 5'
L. CEM/251	5' ATTTT TAGAAGTAAGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3' 3' TAAATCTTCATTCGATCACACACAAGGTTAGAGGATCGGCGCGGAC C 5'
L. 36.8-3	5' ATTTT TAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3' 3' TAAATCTTCATCCGATCACACACAAGGTTAGAGGATCGGCGCGGAC C 5'

FIG. 49G



FIG. 50

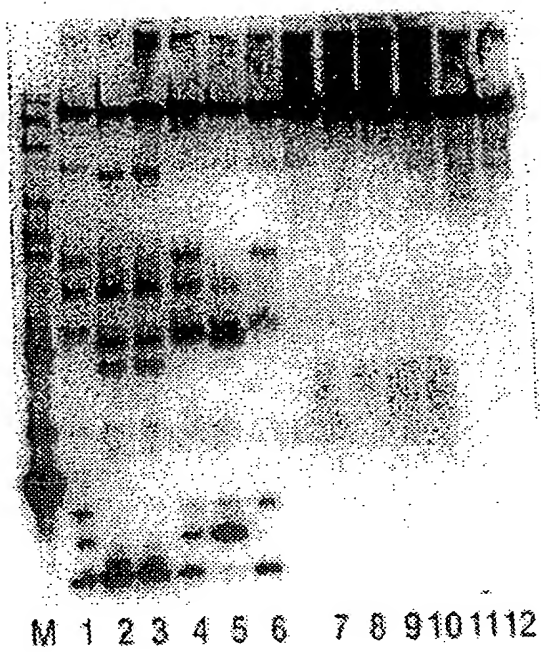


FIG. 51

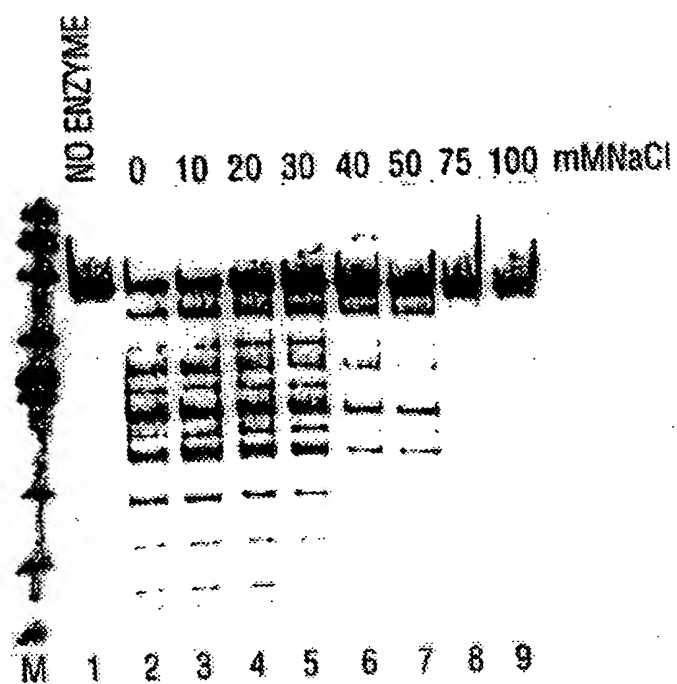


FIG. 52

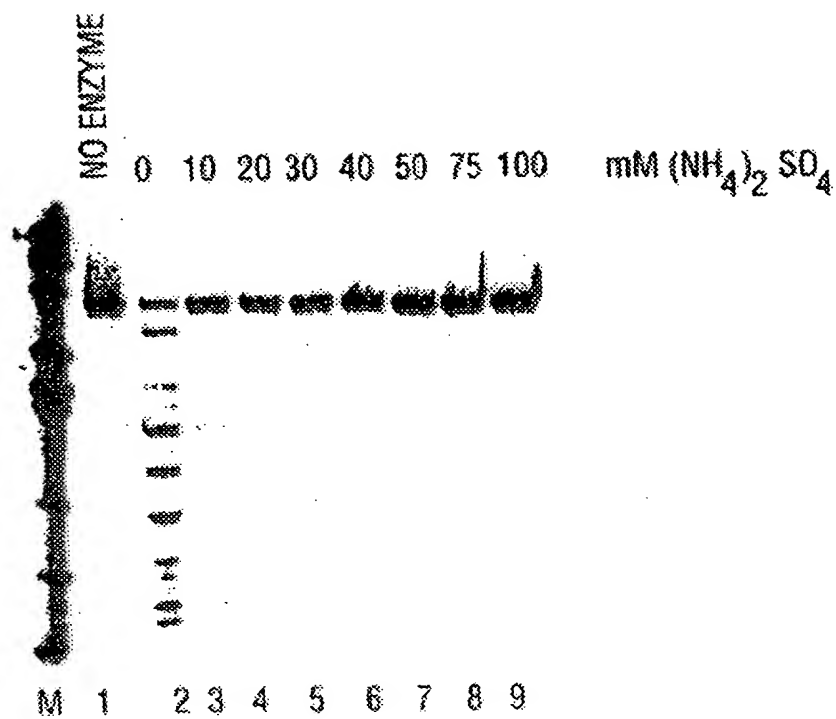


FIG. 53

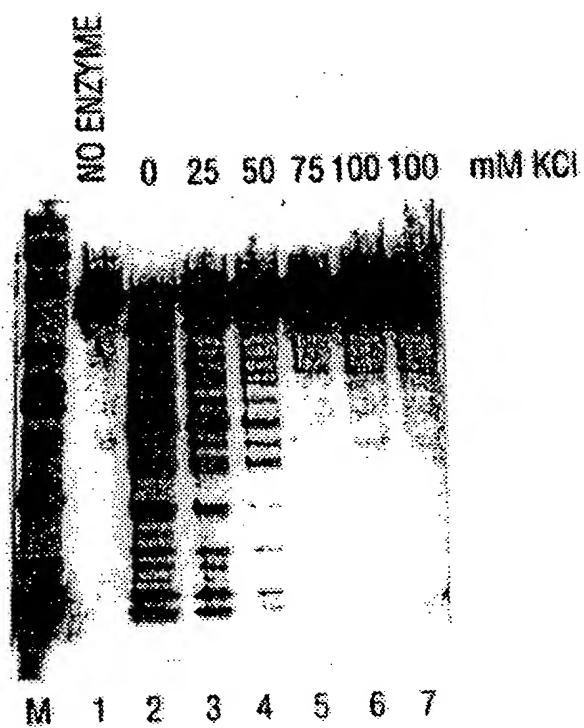


FIG. 54

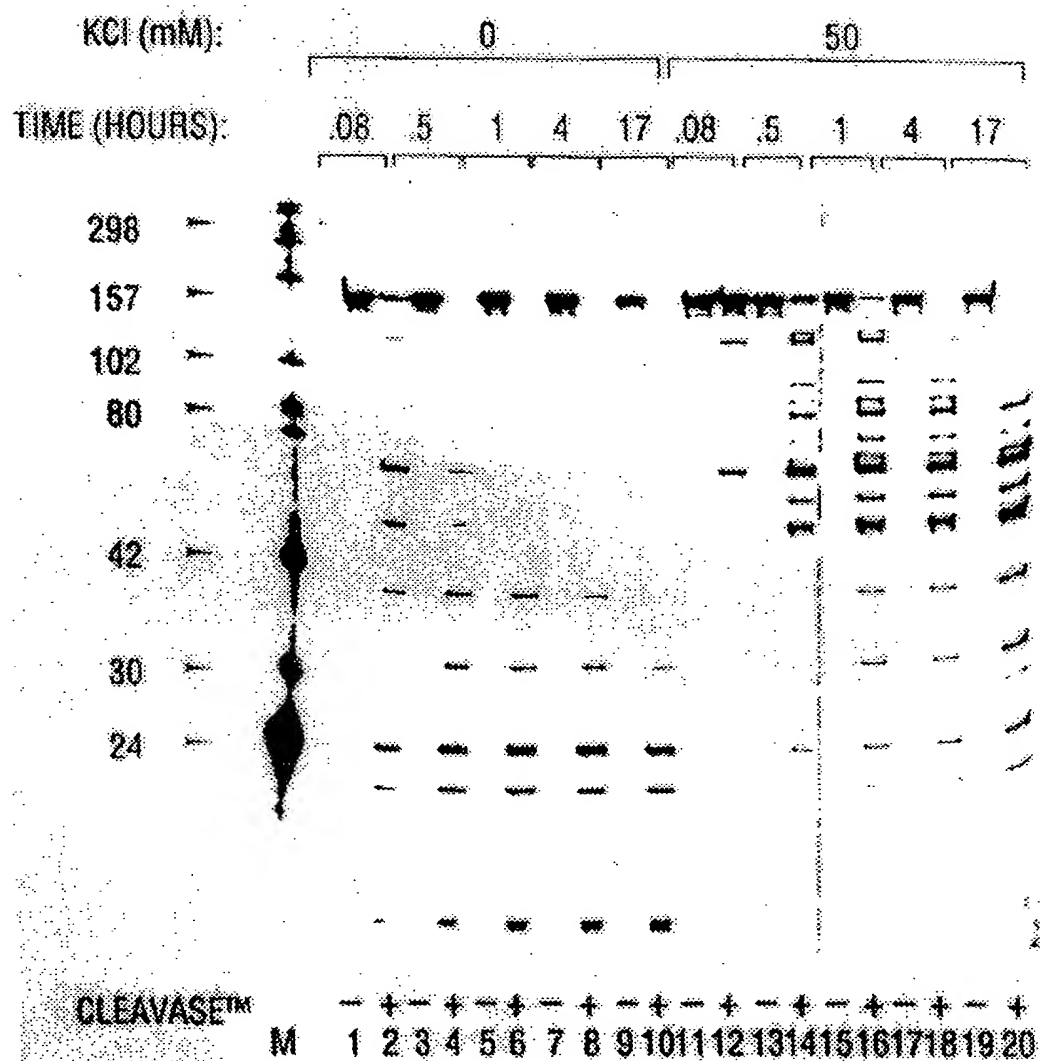


FIG. 55

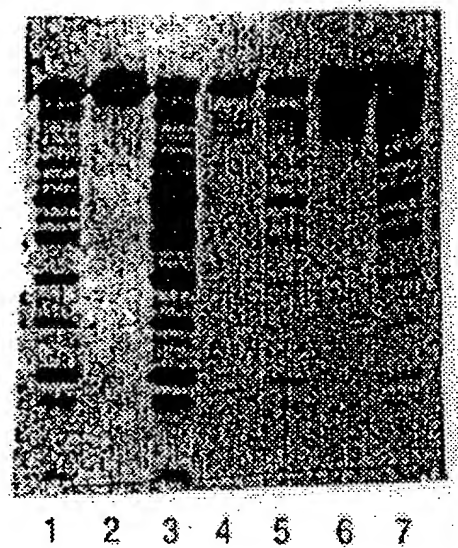


FIG. 56

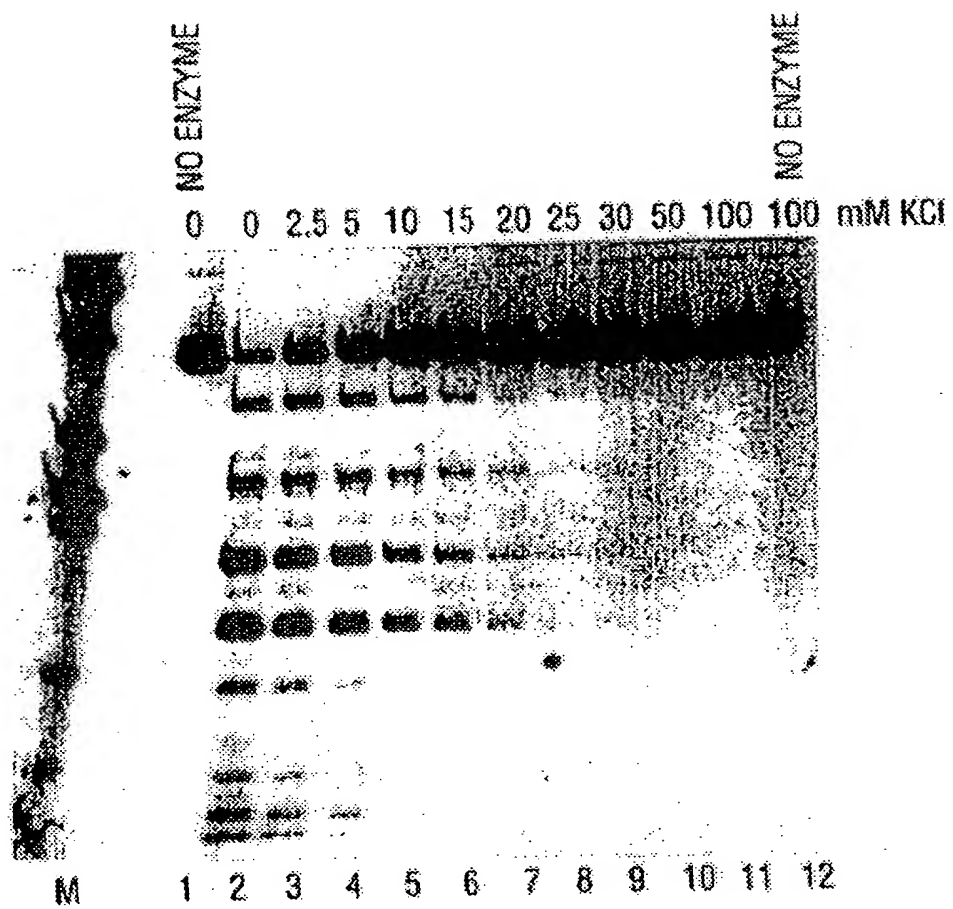


FIG. 57

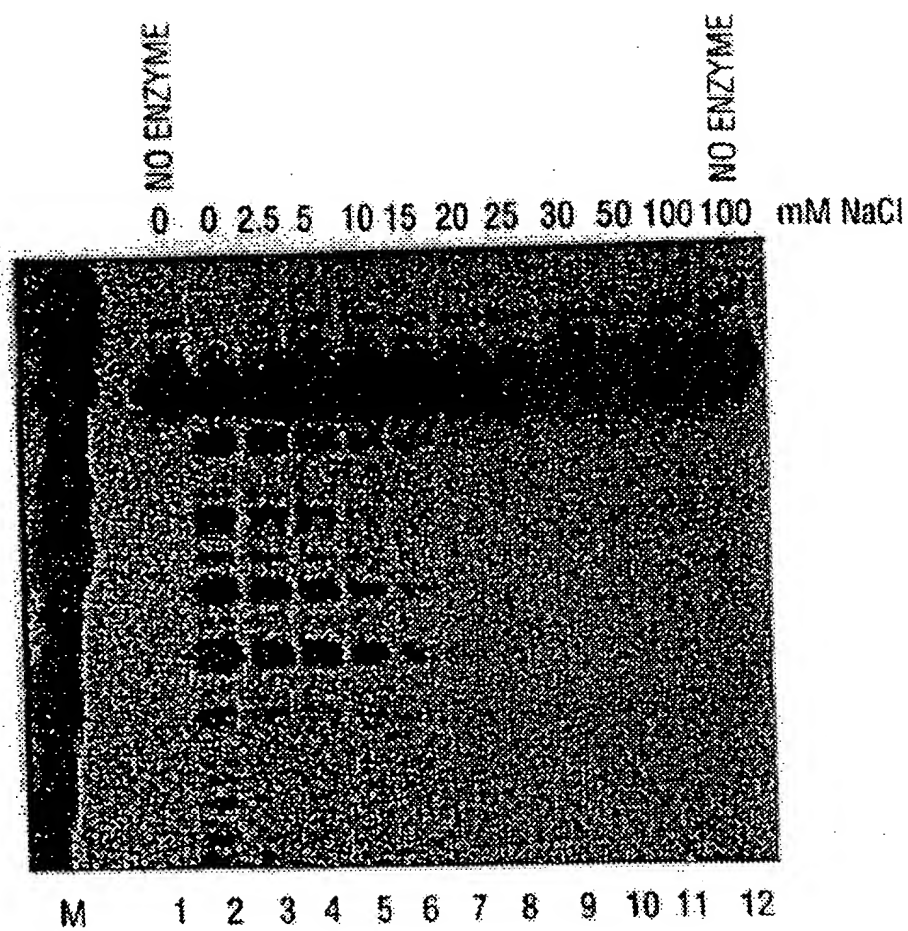


FIG. 58

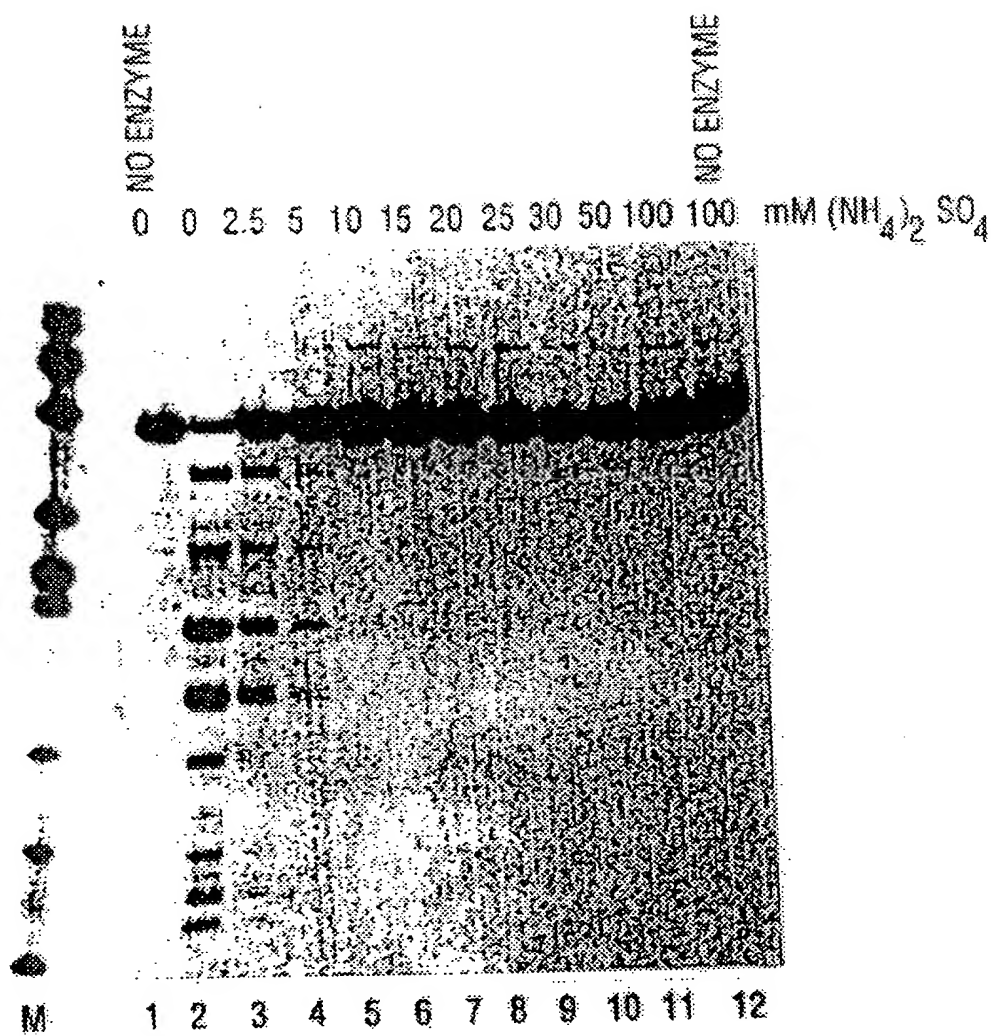


FIG. 59

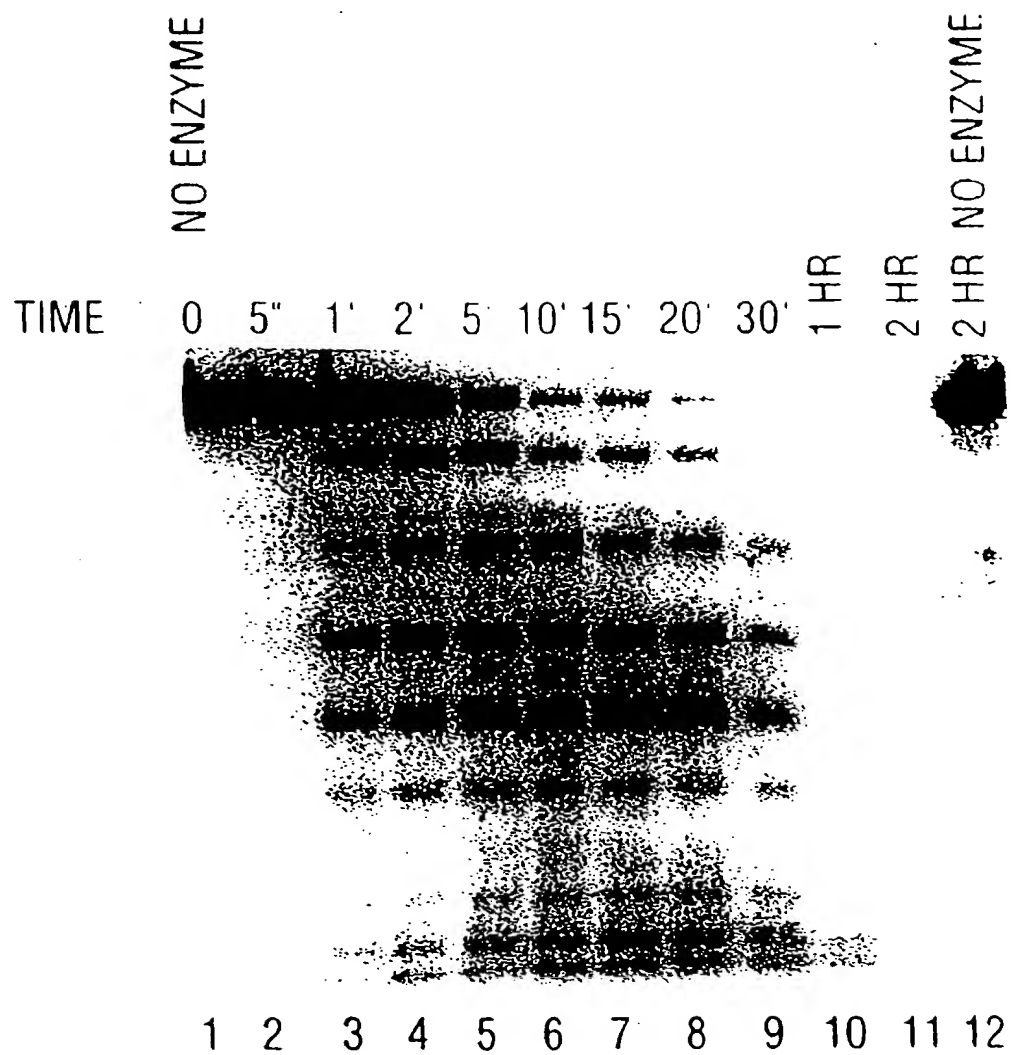


FIG. 60

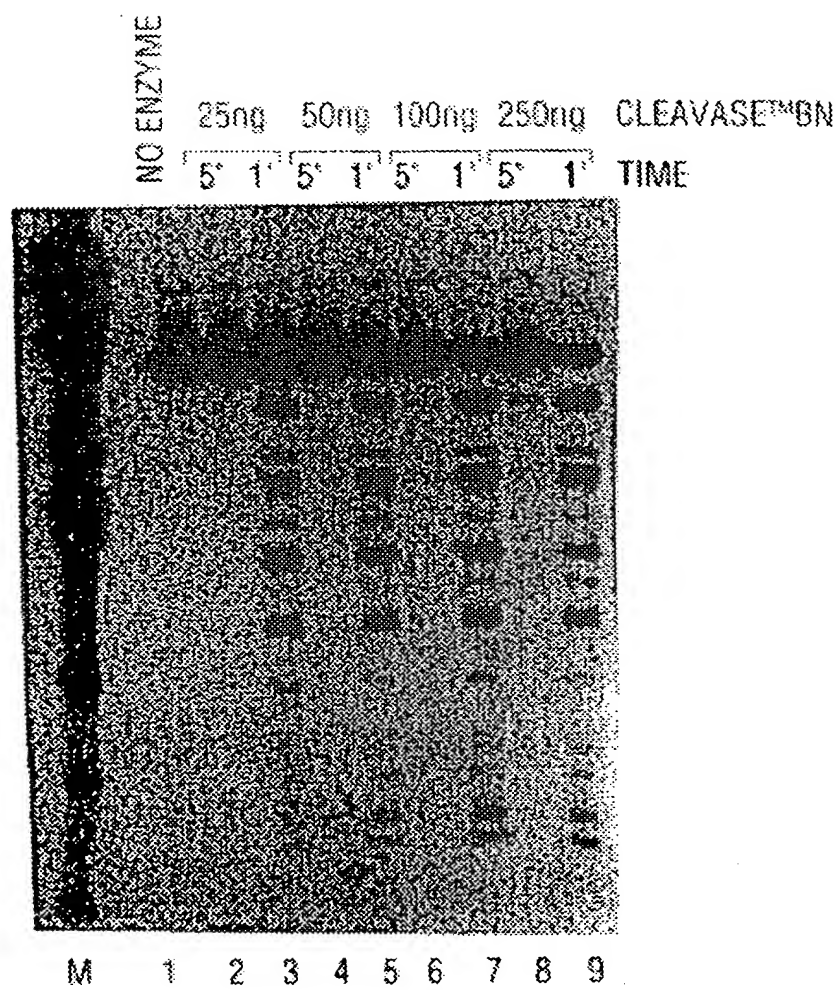


FIG. 61

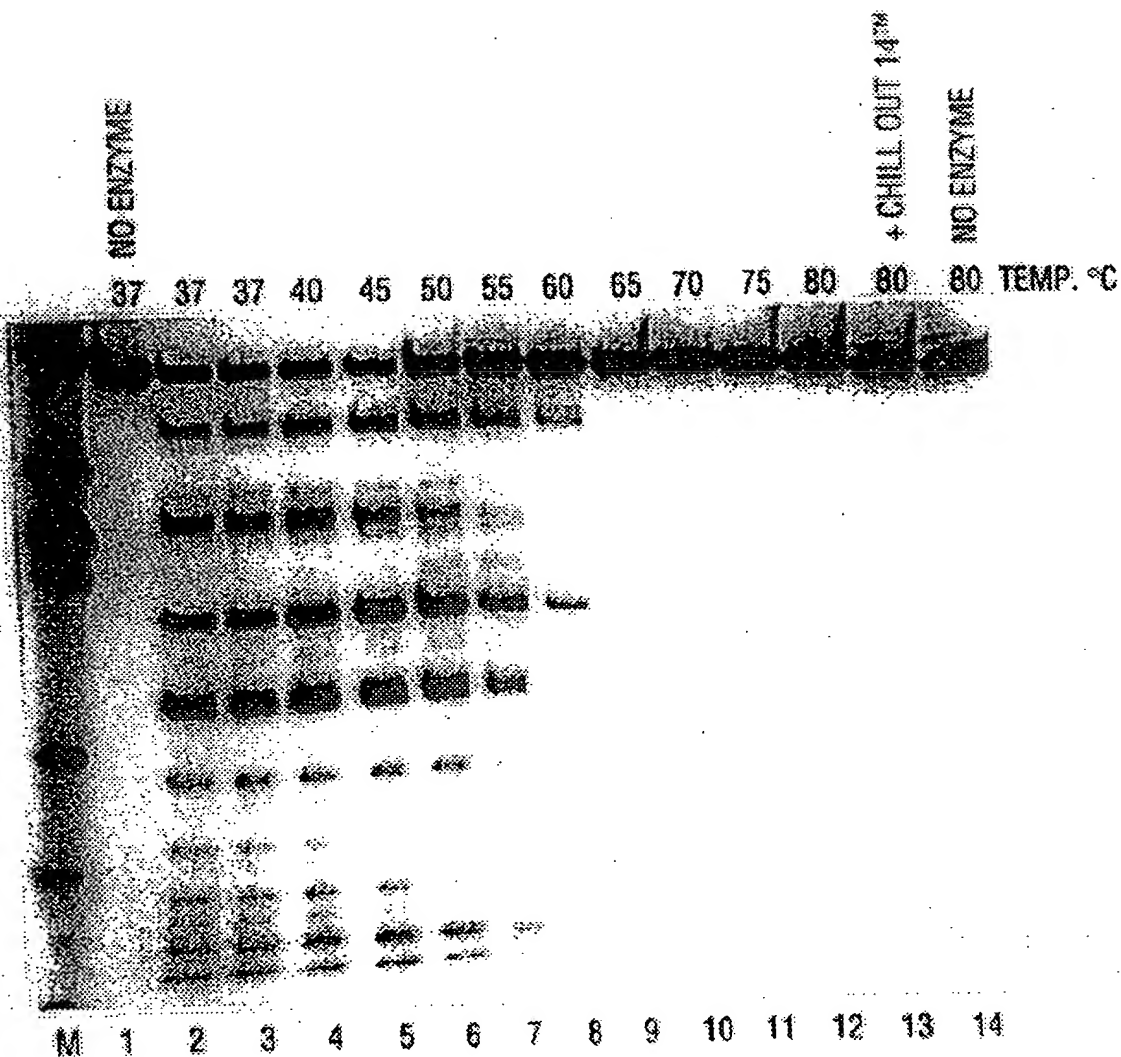


FIG. 62

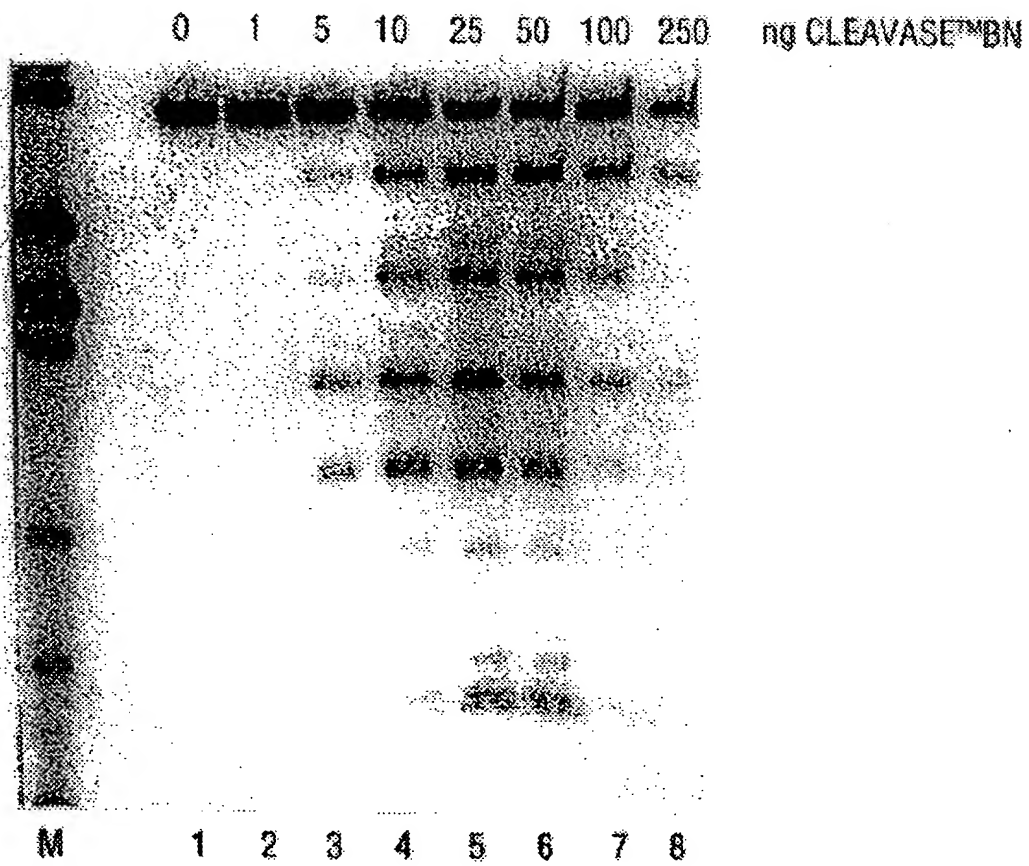


FIG. 63

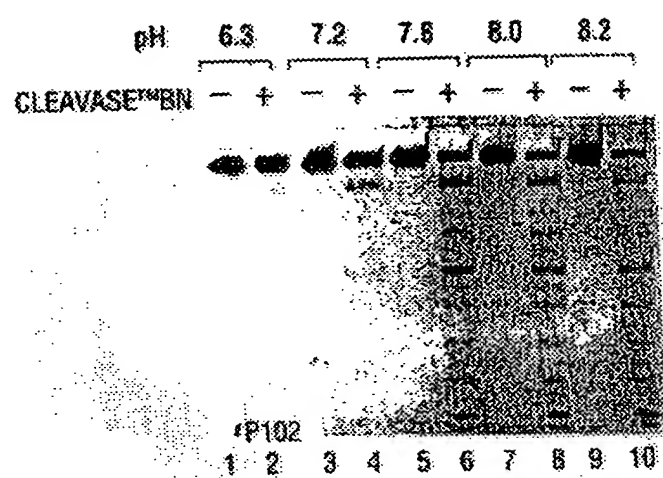


FIG. 64A

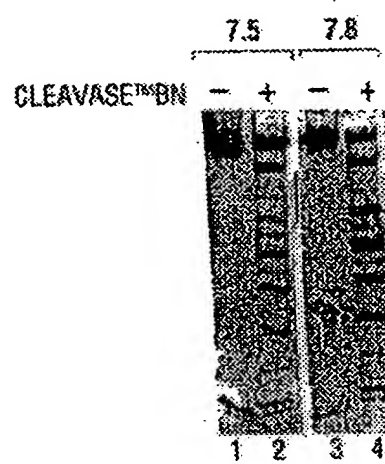


FIG. 64B

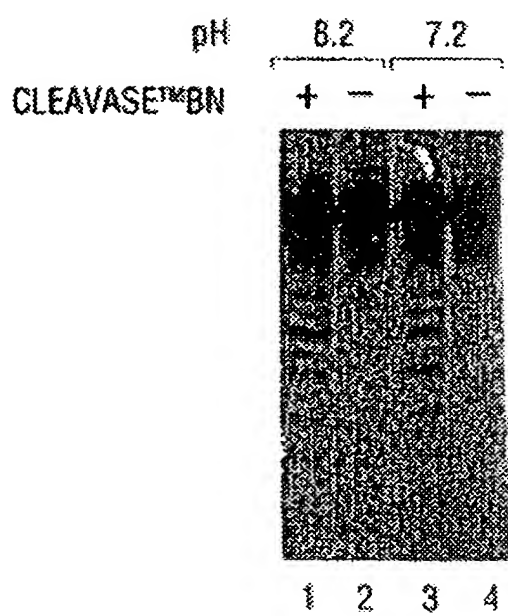


FIG. 65A

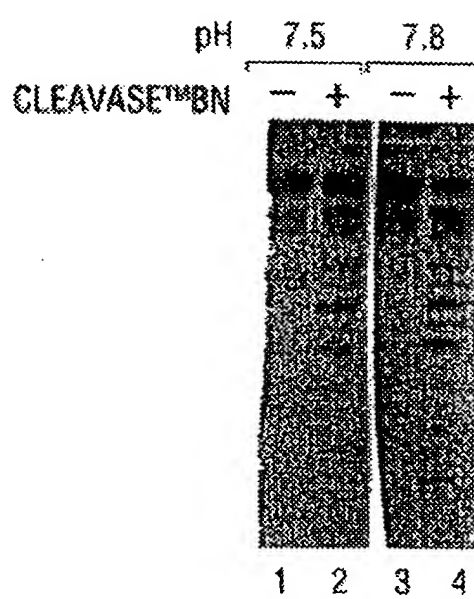


FIG. 65B

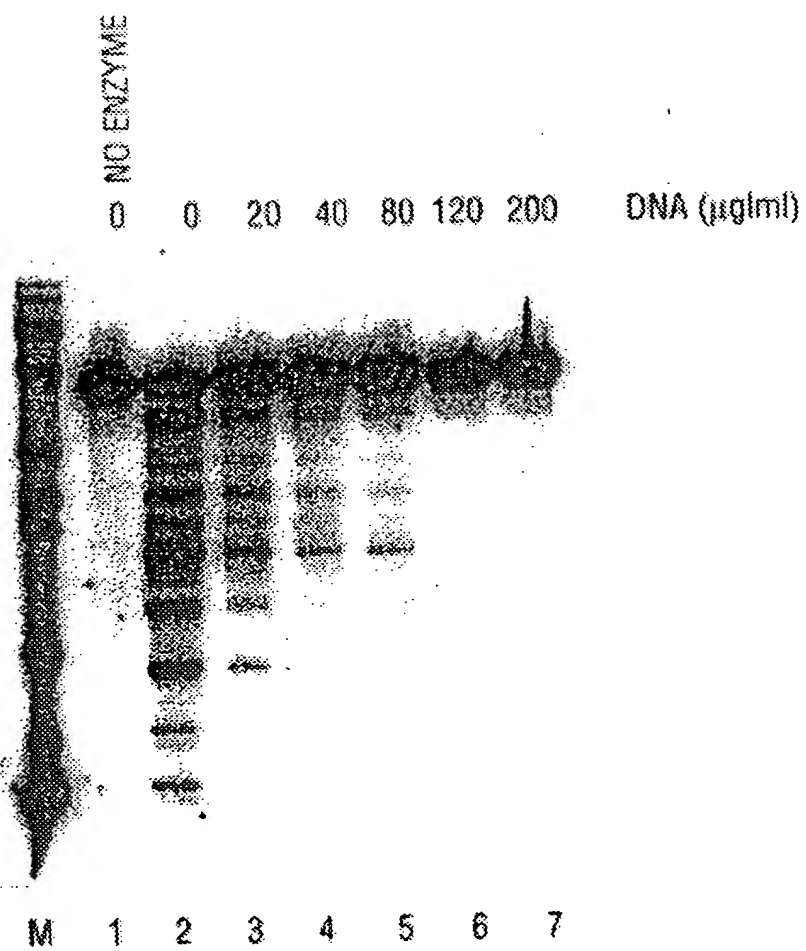


FIG. 66

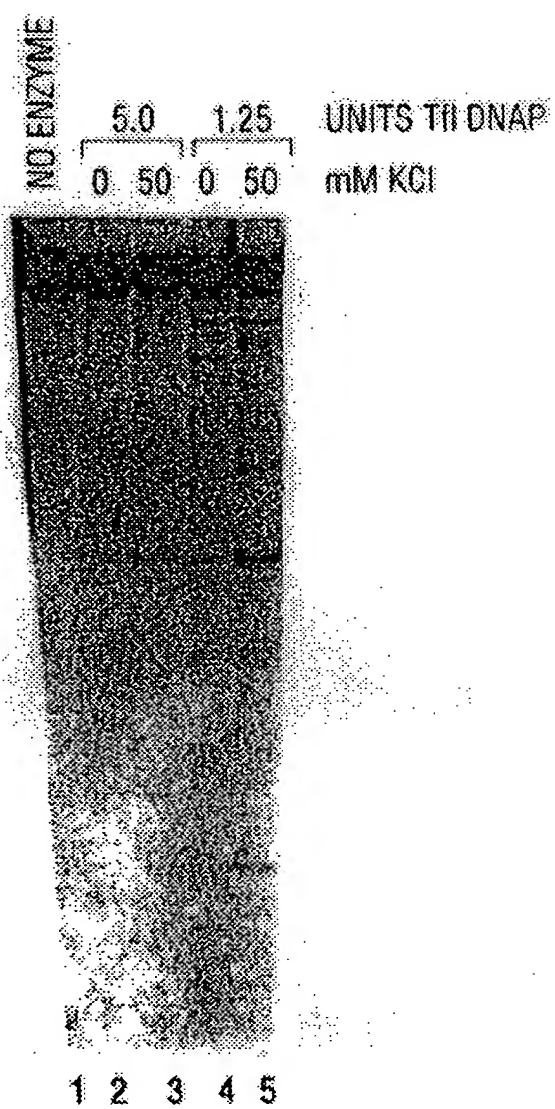


FIG. 67

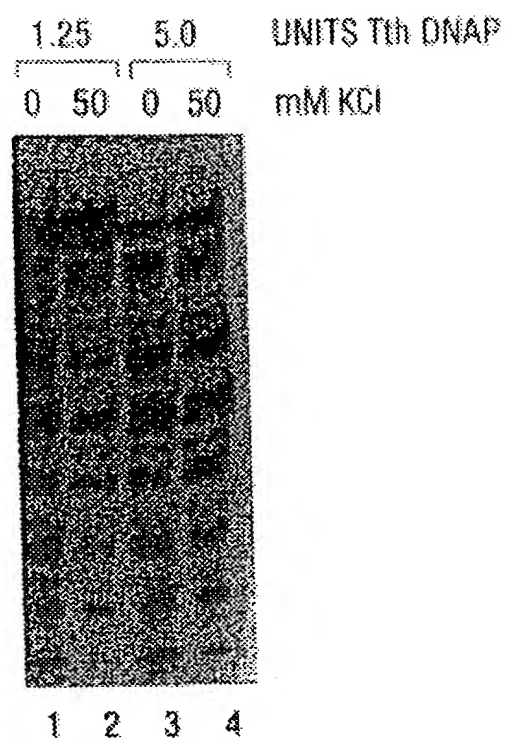


FIG. 68

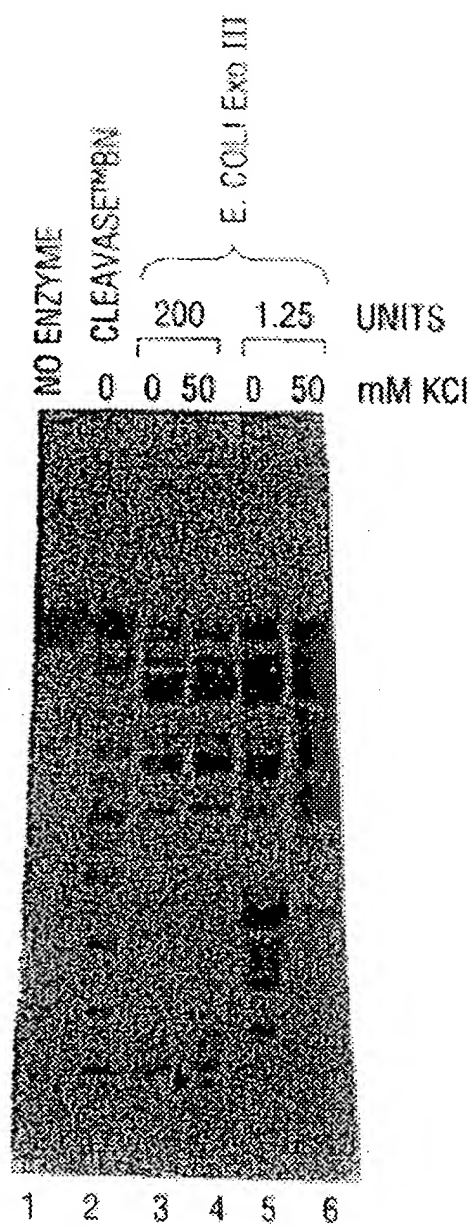


FIG. 69

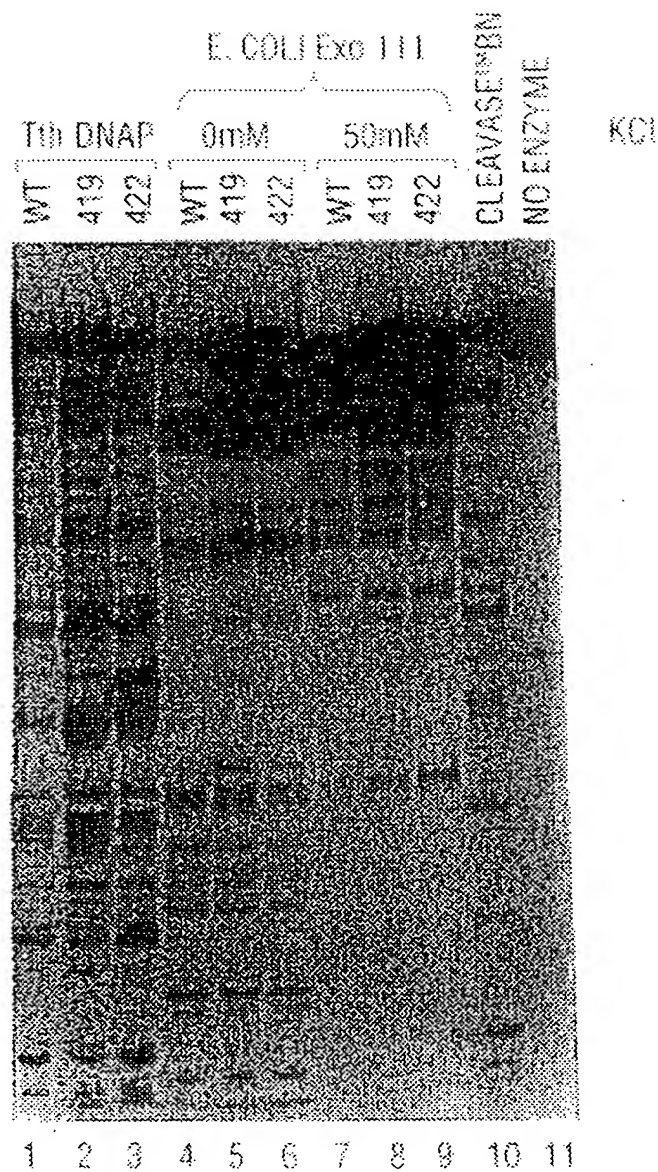
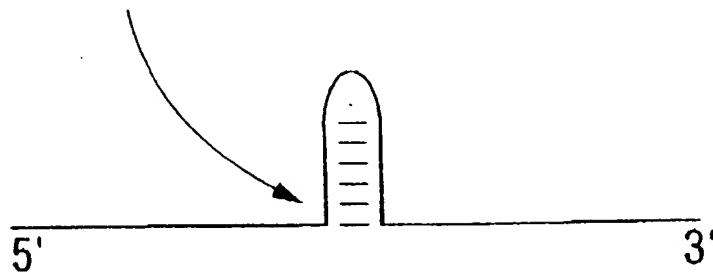


FIG. 70

5' CLEAVAGE SITE



3' CLEAVAGE SITE

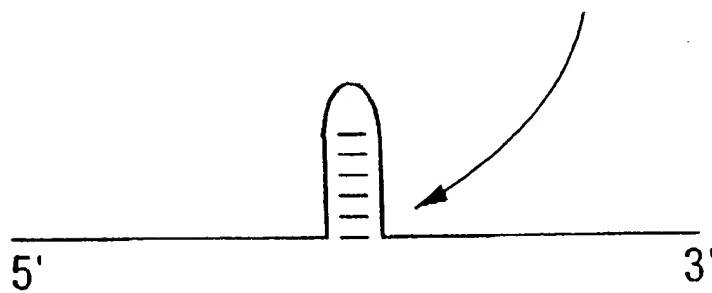


FIG. 71

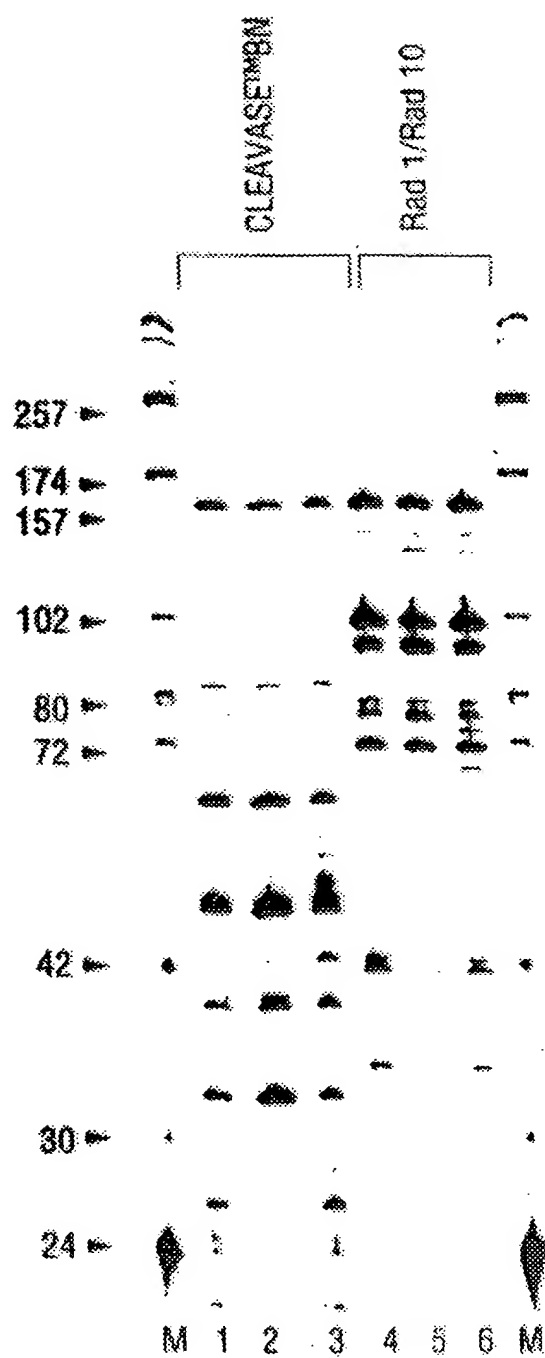


FIG. 72

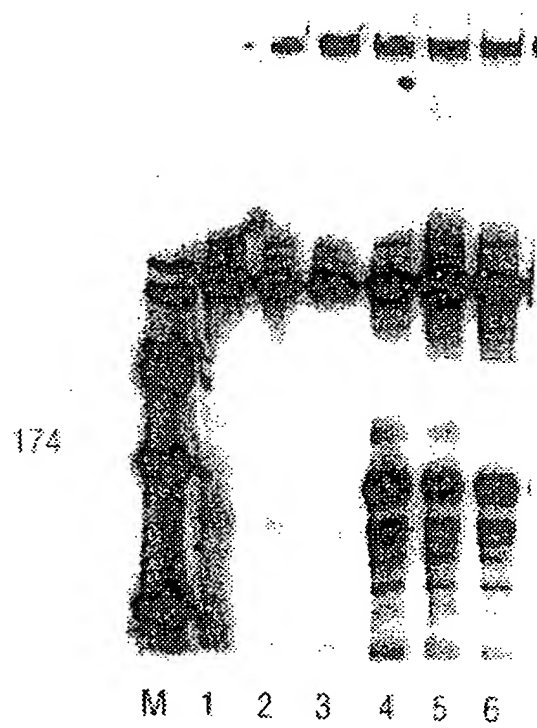


FIG. 73

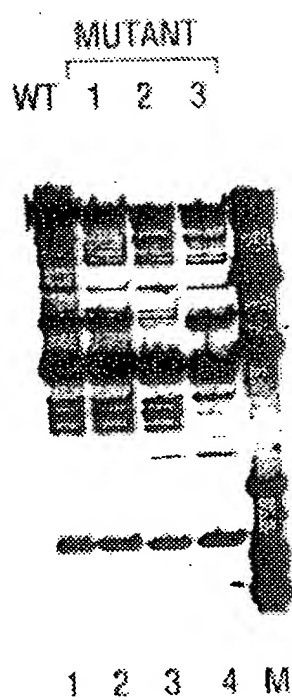


FIG. 74A

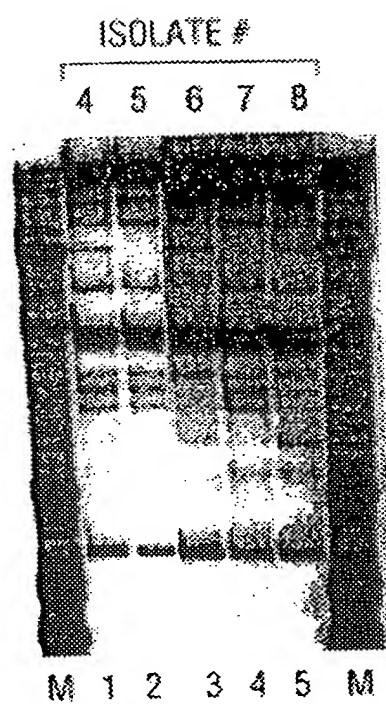


FIG. 74B

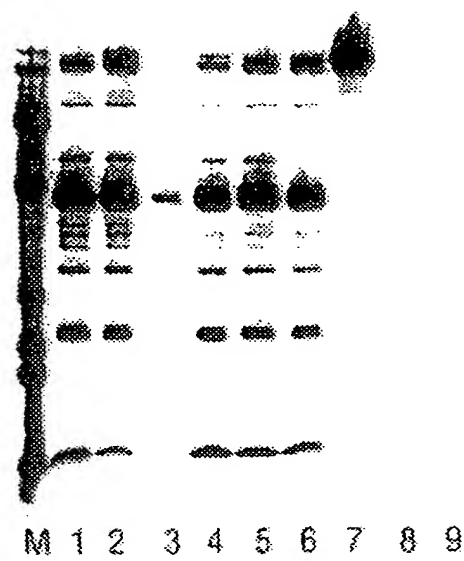


FIG. 75

% OF TOTAL
MUTATIONS

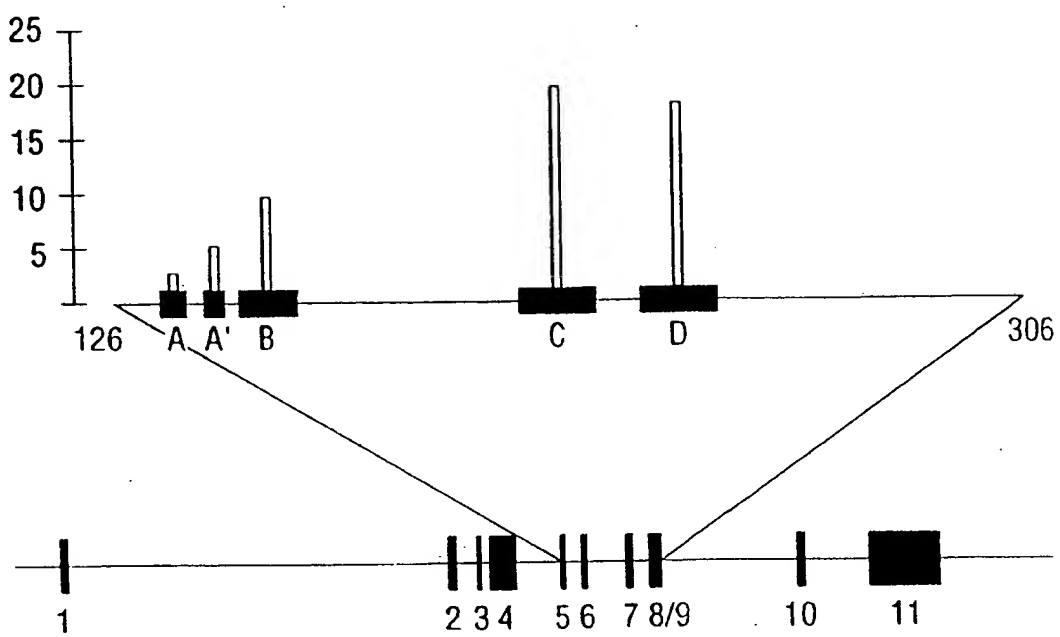


FIG. 76

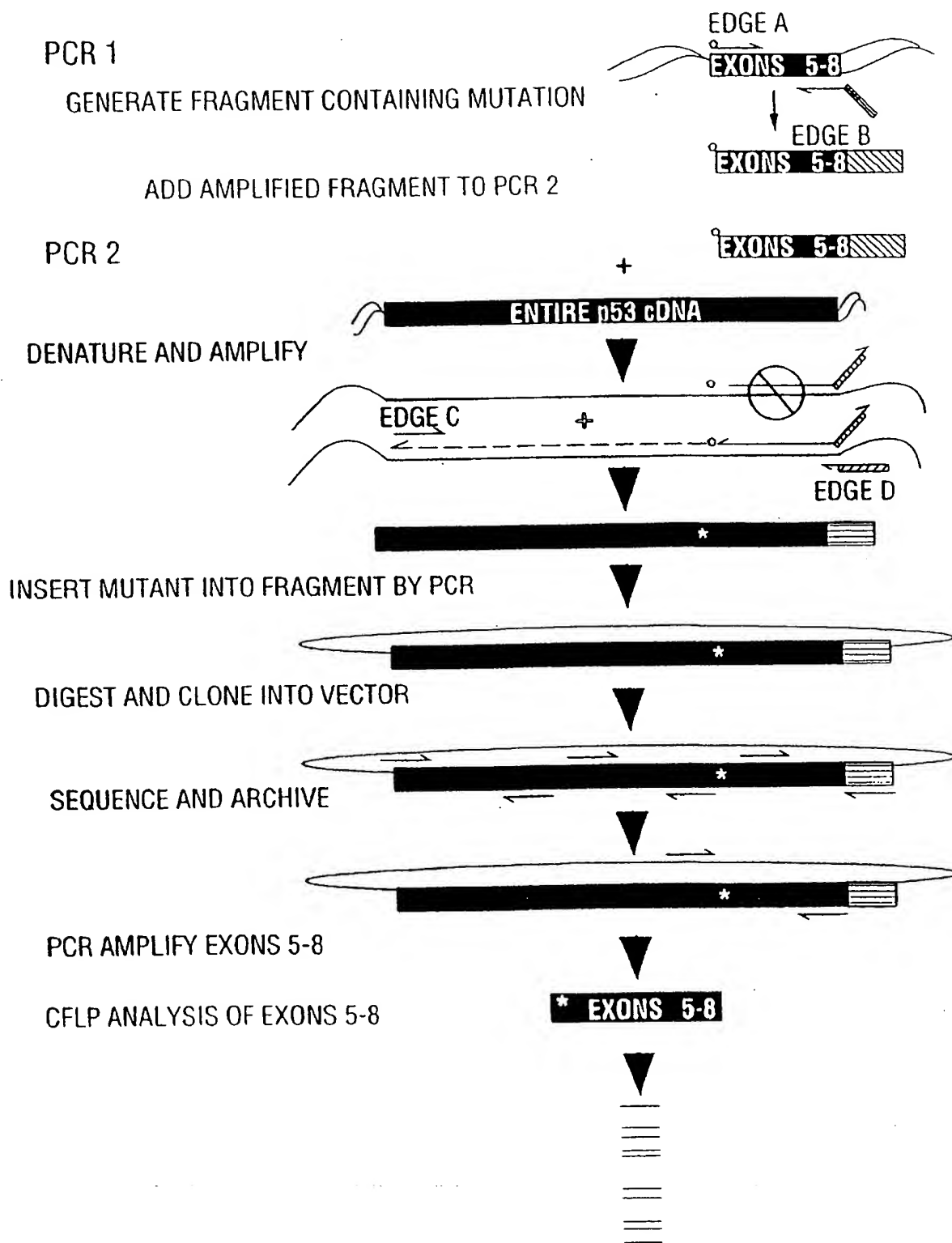


FIG. 77

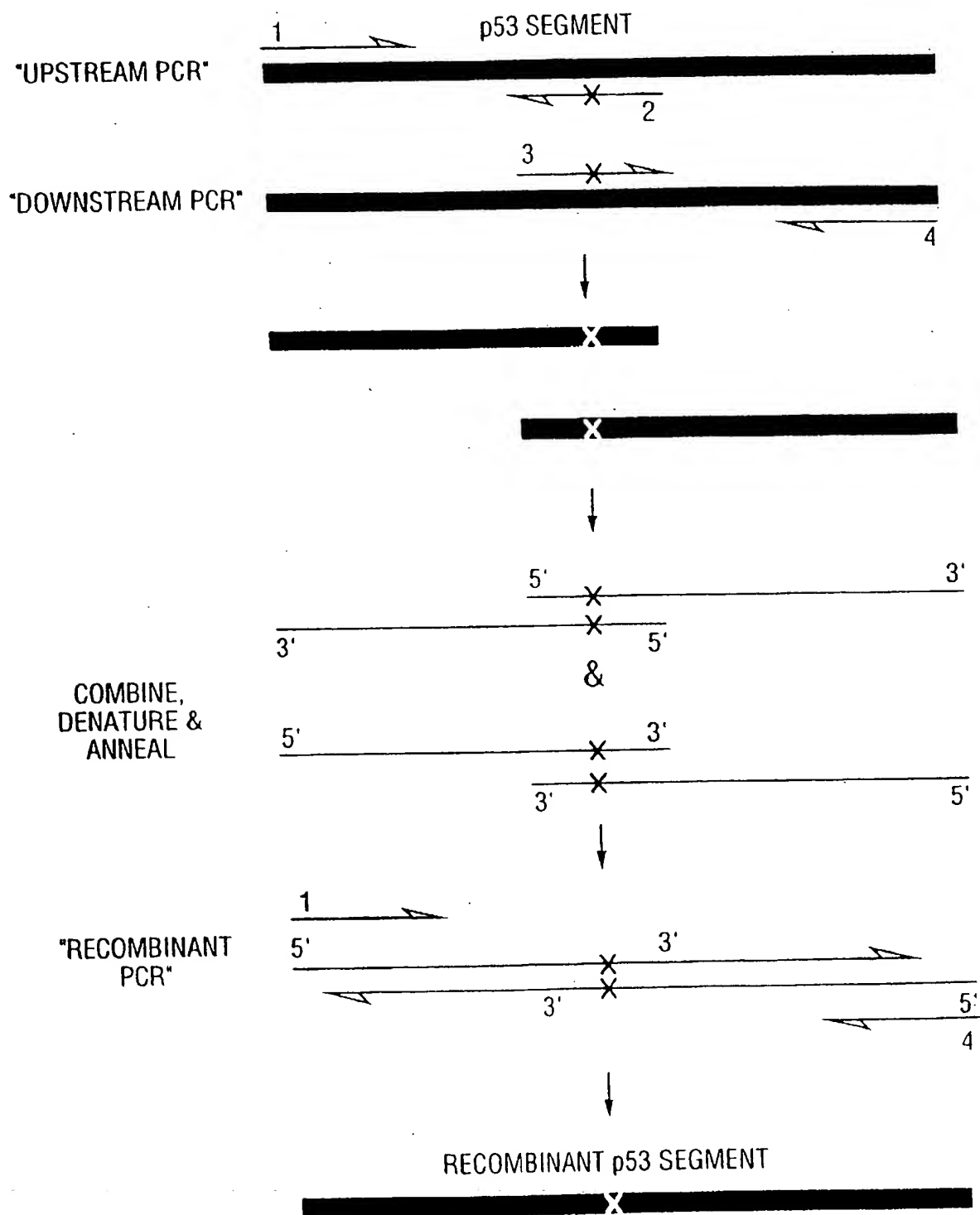


FIG. 78

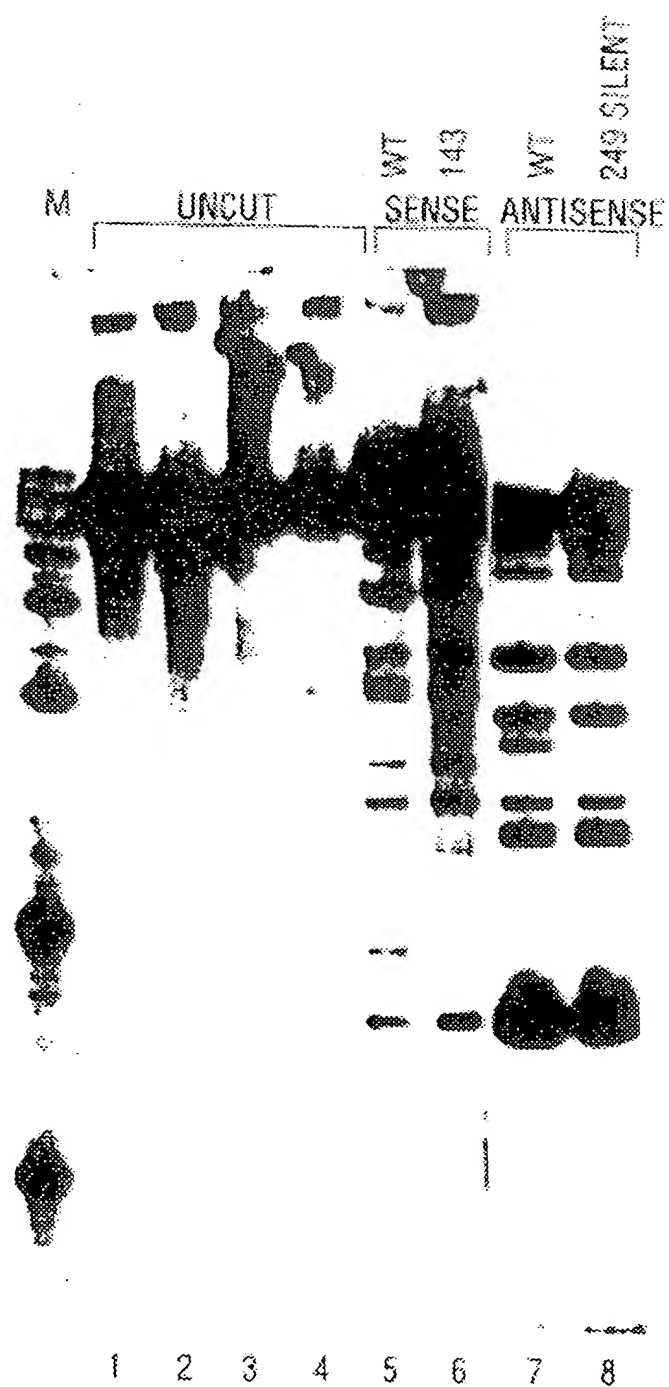


FIG. 79

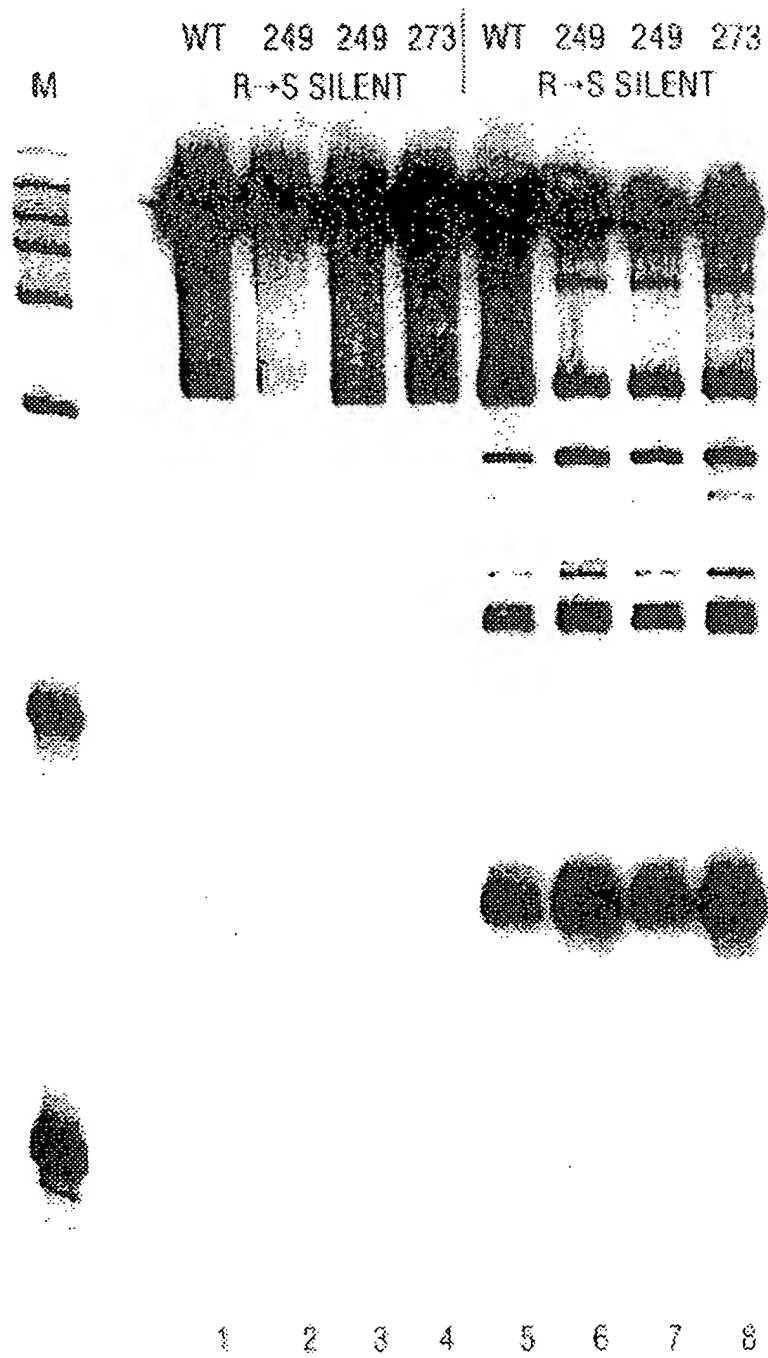


FIG. 80

MIXING PROPORTIONS

M	UNCUT	1	1	1	1	0	2	4	9	WILD TYPE
	WT MUT	0	1	2	9	1	1	1	1	MUTANT

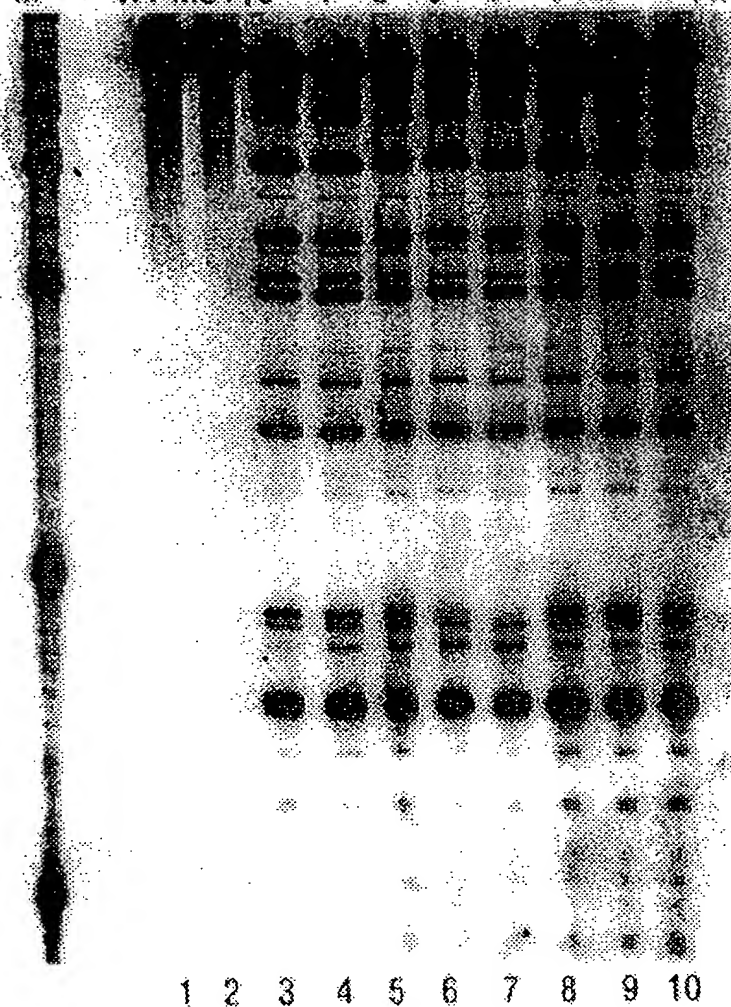


FIG. 81

HCV1.1	(SEQ ID NO:121)	1	CTGTCTTTCAC	GCAGAAAGCG	TCTGGCCATG	GCGTTAGTAT	GAGTGTCTGTG	50
HCV2.1	(SEQ ID NO:122)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV3.1	(SEQ ID NO:123)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV4.2	(SEQ ID NO:124)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV6.1	(SEQ ID NO:125)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV7.1	(SEQ ID NO:126)		CTGTCTTTCAC	GCAGAAAGCG	CTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV1.1		51	CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGGT	CTGCGGAACC	100
HCV2.1			CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV3.1			CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV4.2			CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV6.1			CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV7.1			CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV1.1		101	GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT- <u>AAA</u>	150
HCV2.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT-CAA	
HCV3.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT-CAA	
HCV4.2			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	GTGGAT <u>GIAA</u>	
HCV6.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT- <u>AAA</u>	
HCV7.1			GGTGAGTACA	CCGGAATCGC	<u>IGGGGIGACC</u>	GGGTCCTTTC	TTGGAG-CAA	

FIG. 82A

HCV1.1	151	CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	200
HCV2.1		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV3.1		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCGAGA	CTGCTAGCCG	
HCV4.2		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV6.1		CCCACTCIAT	GCCCGGCCAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV7.1		CCCGCTCAAT	ACCCAGAAAT	TTGGGCGTGC	CCCCGCGAGA	ICACTAGCCG	
HCV1.1	201	AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCTGA	TAGGGTGCTT	250
HCV2.1		AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCTGA	TAGGGTGCTT	
HCV3.1		AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCTGA	TAGGGTGCTT	
HCV4.2		AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCTGA	TAGGGTGCTT	
HCV6.1		AGTAGCGTG	GGTIGCGAAA	GGCCTTGTGG	TACTGCCTGA	TAGGGTGCTT	
HCV7.1		AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCTGA	TAGGGTGCTT	
HCV1.1	251	GCGAGTGCCC	CGGAGGTCT	CGTAGACCGT	GC	282	
HCV2.1		GCGAGTGCCC	CGGAGGTCT	CGTAGACCGT	GC		
HCV3.1		GCGAGTGCCC	CGGAGGTCT	CGTAGACCGT	GC		
HCV4.2		GCGAGTGCCC	CGGAGGTCT	CGTAGACCGT	GC		
HCV6.1		GCGAGTACCC	CGGAGGTCT	CGTAGACCGT	GC		
HCV7.1		GCGAGTGCCC	CGGAGGTCT	CGTAGACCGT	GC		

FIG. 82B

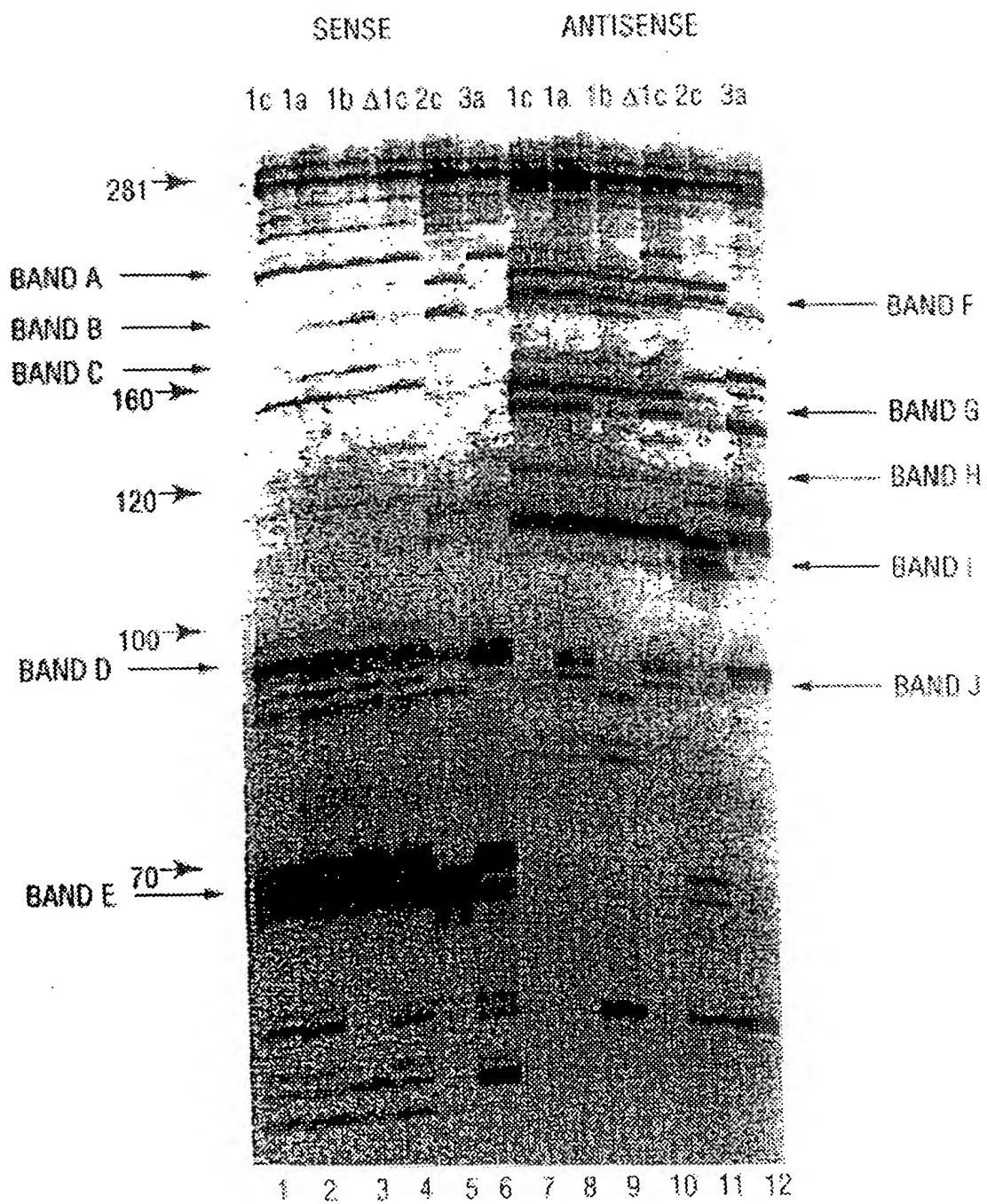


FIG. 83

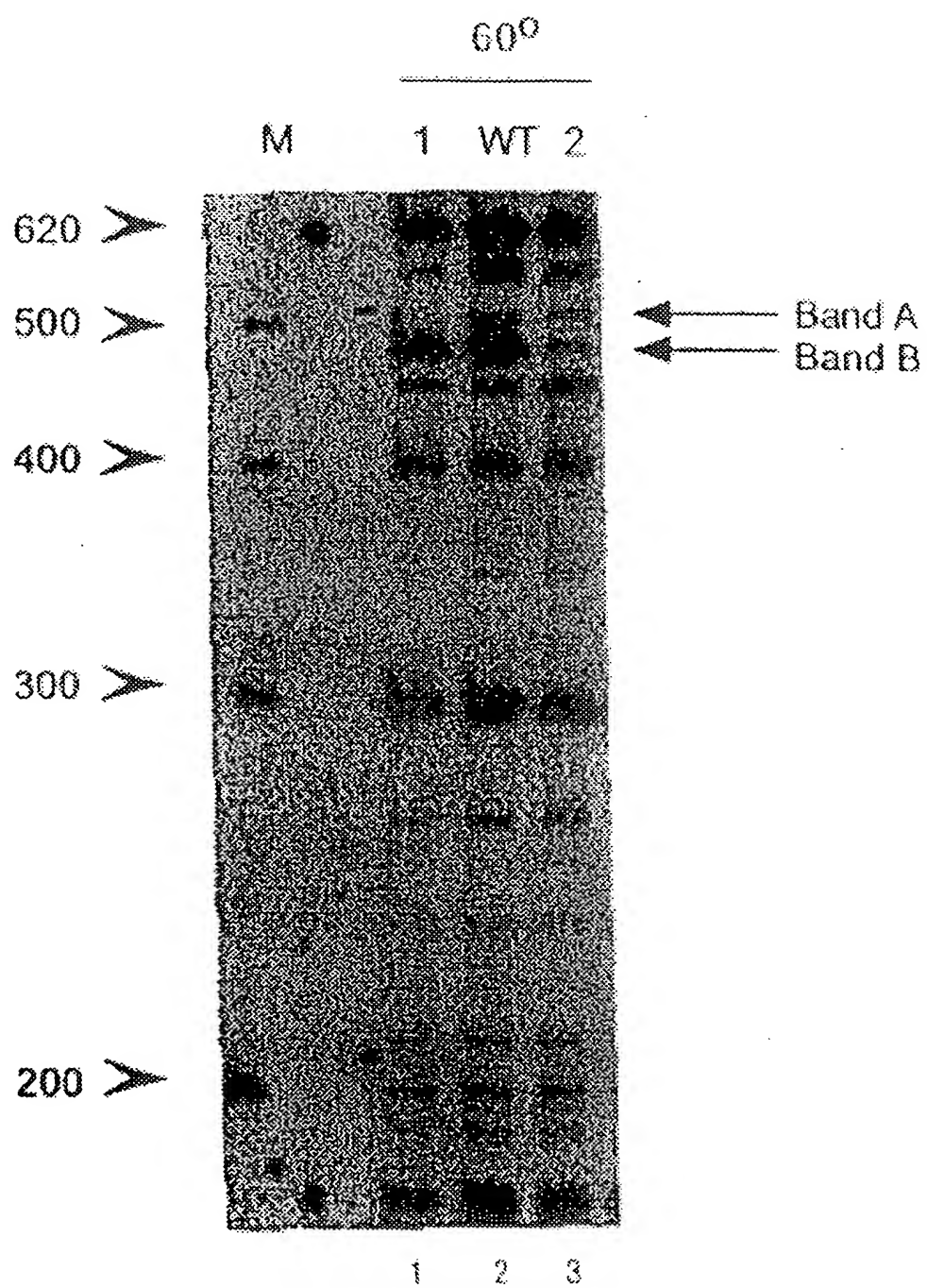


FIG. 84

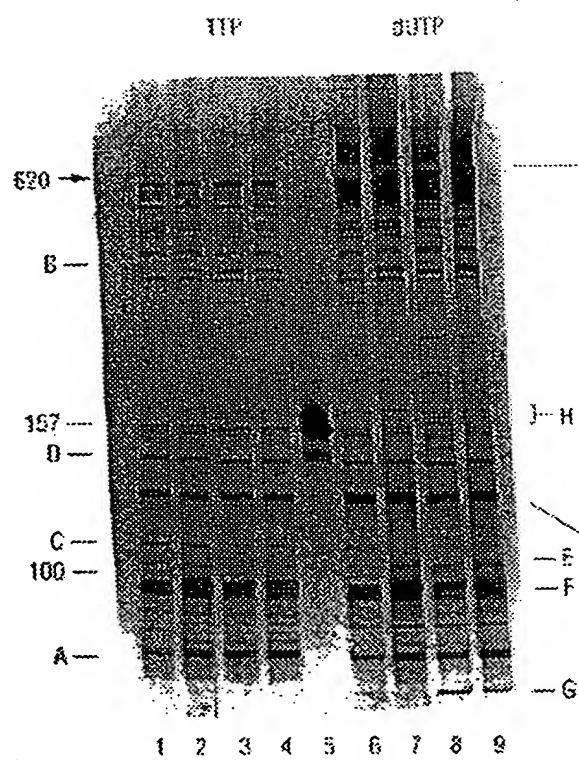


FIG. 85A

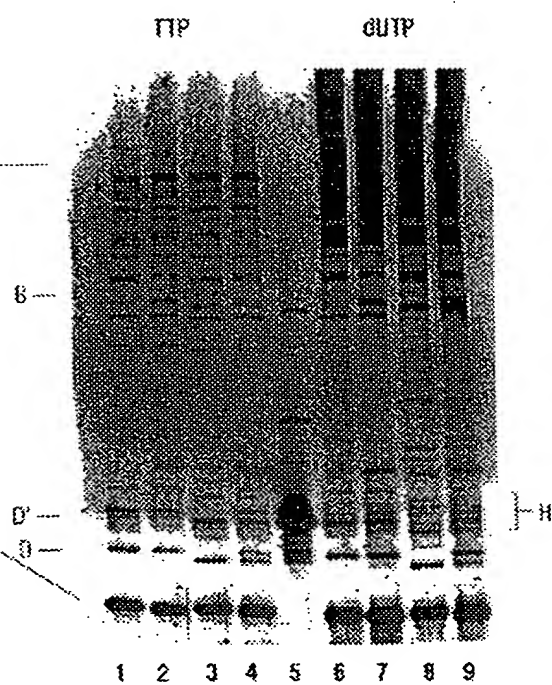


FIG. 85B

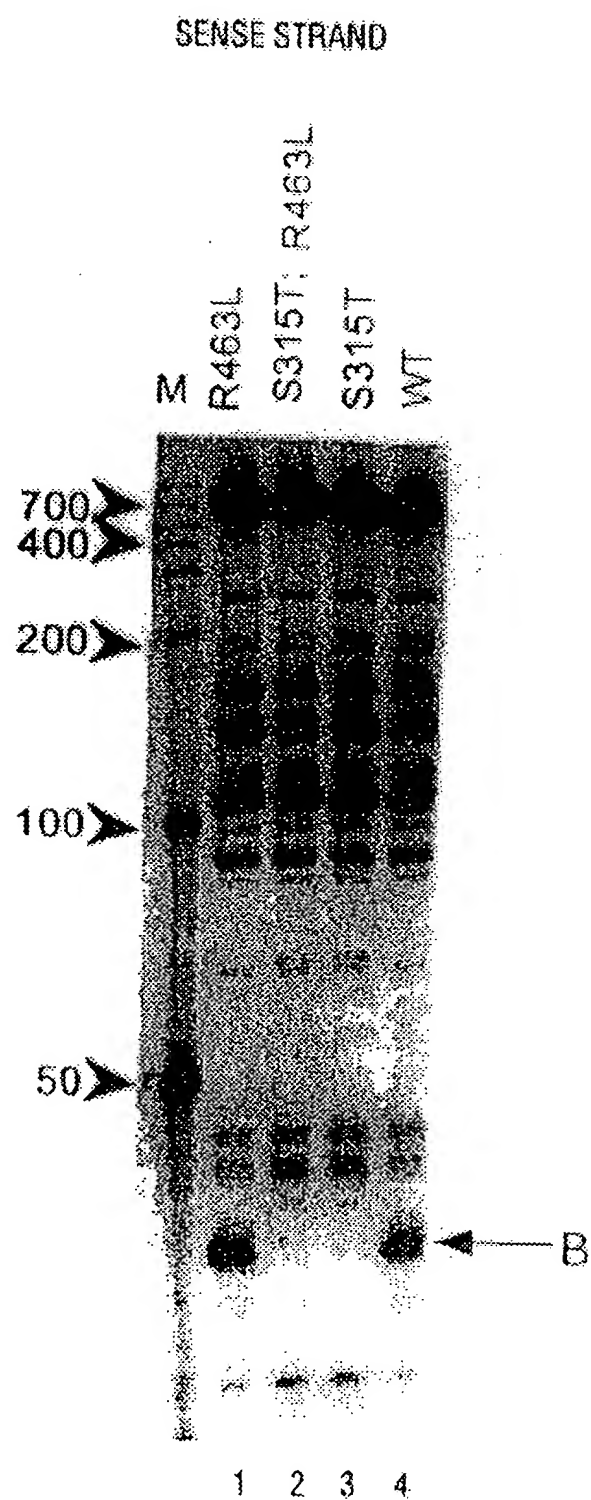


FIG. 86

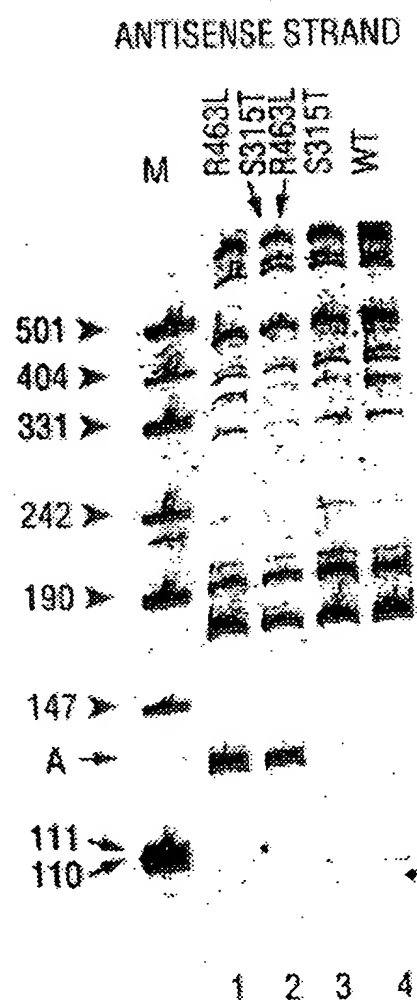


FIG. 87

10	20	30	40	50	60	1638
AGA GTTTGATCCT	GGCTCAG					
AAATTGAAGA	<u>GTTTGATCAT</u>	<u>GGCTCAGATT</u>	GAACGCTGGC	GGCAGGCCCTA	ACACATGCAA	
TTTAACCTTCT	CAAACTAGTA	CCGAGTCTAA	CTTGCGACCG	CCGTCCGGAT	TGTGTACGTT	
70	80	90	100	110	120	ER10
GTCGAACGGT	AACAGGAAGA	AGCTTGCTTC	TTTGCTGACG	AGTGCGGGAC	<u>GGTGAGIAA</u>	
CAGCTTGCCA	TTGTCCTTCT	TCGAACGAAG	AAACGACTGC	TCACCGCCTG	CCCACCTATT	
130	140	150	160	170	180	
TGTCTGGGAA	ACTGCCCTGAT	GGAGGGGGAT	AACTACTGGA	AACGGTAGCT	AATACCGCAT	
ACAGACCCCT	TGACGGACTA	CCTCCCCCTA	TTGATGACCT	TTGCCATCGA	TTATGGCGTA	
190	200	210	220	230	240	
AACGTCGCAA	GACCAAAGAG	GGGGACCTTC	GGGCCTCTTG	CCATCGGATG	TGCCCCAGATG	
TTGCAGCGTT	CTGGTTTCTC	CCCCTGGAAG	CCCGGAGAAC	GGTAGCCTAC	ACGGGTCTAC	
250	260	270	280	290	300	
GGATTAGCTA	GTAGGTGGGG	TAACGGCTCA	CCTAGGCGAC	GATCCCTAGC	TGGTCTGAGA	
CCTAATCGAT	CATCCACCCC	ATTGCCGAGT	GGATCCGCTG	CTAGGGATCG	ACCAGACTCT	
310	320	330	340	350	360	
GGATGACCAG	CCACACTGGA	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTGG	
CCTACTGGTC	GGTGTGACCT	TGACTCTGTG	CCAGGTCTGA	<u>GGATGCCCTC</u>	<u>CGTCGTCACC</u>	
			TGA	GGATGCCCTC	CGTCGTC	1659

FIG. 88A

370	380	390	400	410	420
GGAATATTGC	ACAATGGGCG	CAAGCCTGAT	GCAGCCATGC	CGCGTGTATG	AAGAAGGCCT
CCTTATAACG	TGTTACCCGC	GTTCGGAATA	CGTCGGTACG	CGCACATAC	TTCTTCCGGA
430	440	450	460	470	480
TCGGGTTGTA	AAGTACTTTC	AGCGGGGAGG	AAGGGAGTAA	AGTTAATACC	TTTGCTCATT
AGCCCCAACAT	TTCATGAAAG	TCGCCCCCTCC	TTCCCTCATT	TCAATTATGG	AAACGAGTAA
490	500	510	520	530	540
GACGTTACCC	GCAGAAAGAAG	CACCGGCTAA	CTCCGTGCCA	GCAGCCGCGG	TAATACGGAG
CTGCAATGGG	CGTCTTCTTC	GTGGCCGATT	GAGGCACGGT	CGTCGGCGCC	ATTATGCCTC
550	560	570	580	590	600
GGTGCAAGCG	TTAATCGGAA	TTACTGGGCG	TAAAGCGCAC	GCAGGCGGTT	TGTTAAGTCA
CCACGTTTCG	AATTAGCCTT	AATGACCCGC	ATTTGCGGTG	CGTCCGCCAA	ACAATTTCAGT
610	620	630	640	650	660
GATGTGAAAT	CCCCGGGCTC	AACCTGGGAA	CTGCATCTGA	TACTGGCAAG	CTTGAGTCTC
CTACACTTTA	GGGGCCCGAG	TTGGACCCCT	GACGTAGACT	ATGACCGTTC	GAACTCAGAG
670	680	690	700	710	720
GTAGAGGGGG	GTAGAATTCC	AGGTGTAGCG	GTGAAATGCG	TAGAGATCTC	GAGGAATACC
CATCTCCCCC	CATCTTAAGG	TCCACATCGC	CACTTTACGC	ATCTCTAGAC	CTCCTTATGG
730	740	750	760	770	780
GGTGGCGAAG	GCGGCCCCCT	GGACGAAGAC	TGACGCTCAG	GTGCGAAAGC	GTGGGGAGCA
CCACCGCTTC	CGCCGGGGGA	CCTGCTTCTG	ACTGCGAGTC	CACGCTTTCG	CACCCCTCGT

FIG. 88B

	790	800	810	820	830	840
AACAGGATTA	GATACCCTGG	TAGTCCACGC	CGTAAACGAT	GTCGACTTGG	AGGTGTGTCC	
TTGTCCTAAT	CTATGGGACC	ATCAGGTGG	GCATTTGCTA	CAGCTGAACC	TCCAACACGG	
850	860	870	880	890	900	
CTTGAGGCCGT	GGCTTCCGGA	GCTAACGCCGT	TAAGTCGACC	GCCTGGGGAG	TACGGCCGCA	
GAACTCCGCA	CCGAAGGCCT	CGATTGCGCA	ATTCAGCTGG	CGGACCCCTC	ATGCCGGCGT	
910	920	930	940	950	960	
AGGTTAAAAC	TCAAATGAAT	TGACGGGGGC	CCGCACAAGC	GGTGGAGCAT	GTGGTTTTAAT	
TCCAAATTTTG	AGTTTACTTA	ACTGCCCCCG	GGCGTGTTCTG	CCACCTCGTA	CACCAAATTA	
970	980	990	1000	1010	1020	
TCGATGCAAC	GCGAAGAACC	TTACCTGGTC	TTGACATCCA	CGGAAGTTTT	CAGAGATGAG	
AGCTACGTTG	CGCTTCTTGG	AATGGACCAG	AACTGTAGGT	GCCTTCAAAA	GTCTCTACTC	
1030	1040	1050	1060	1070	1080	
AATGTGCCCT	CGGGAACCGT	GAGACAGGTG	CTGCATGGCT	GTCGTCAGCT	CGTGTGTGTGA	
TTACACGGAA	GCCCCTTGGCA	CTCTGTCCAC	GACGTACCGA	CAGCAGTCGA	GCACAACACT	
1090	1100	1110	1120	1130	1140	
	GC	AACGAGCGCA	ACCC			
AATGTTGGGT	TAAGTCCCGC	AACGAGCGCA	ACCCTTATCC	TTTGTTGCCA	GCGGTCGGGC	
TTACAACCCA	ATTCAGGGCG	TTGCTCGCGT	TGGGAATAGG	AAACAACGGT	CGCCAGGCCG	
1150	1160	1170	1180	1190	1200	
				ATG	ACGTCAAGTC	
				ATG	ACGTCAAGTC	
CGGGAACCTCA	AAGGAGACTG	CCAGTGATAA	ACTGGAGGAA	GGTGGGGATG	ACGTCAAGTC	
GCCCTTGAGT	TTCTCTGAC	GGTCACTATT	TGACCTCCTT	CCACCCCTAC	TGCAGTTTCAG	

FIG. 88C

1210	1220	1230	1240	1250	1260	
ATCATGGCCC	TTA					SB-3
ATCATGGCCC	TTACGA					SB-4
ATCATGGCCC	TTACGACCAG	GGCTACACAC	GTGCTACAAT	GGCGCATACA	AAGAGAACGG	
<u>TAGTACCGGG</u>	<u>AATGCTGGTC</u>	CCGATGTGTG	CACGATGTTA	CCGCGTATGT	TTCTCTTTCGC	
1270	1280	1290	1300	1310	1320	
ACCTCGCGAG	AGCAAGCGGA	CCTCATAAAG	TGCGTCGTAG	TCCGGATTGG	AGTCTGCAAC	
TGGAGCGCTC	TCGTTGCCT	GGAGTATTTC	ACGCAGCATC	AGGCCTAACCC	TCAGACGTTG	
1330	1340	1350	1360	1370	1380	
TCGACTCCAT	GAAGTCGGAA	TCGCTAGTAA	TCGTGGATCA	GAATGCCACG	GTGAATACGT	
AGCTGAGGTA	CTTCAGCCTT	AGCGATCATT	AGCACCTAGT	CTTACGGTGC	<u>CACIIATGCA</u>	1743
				GC	CACTTATGCA	
1390	1400	1410	1420	1430	1440	
TCCCGGGCCT	TGTACACACC	GCCCCGTACA	CCATGGGAGT	GGGTTGCAAA	AGAAGTAGGT	
<u>AGGGCCCCGA</u>	<u>ACATGTGTGG</u>	CGGGCAGTGT	GGTACCCCTCA	CCCAACGTTT	TCTTCATCCA	1743
AGGGCCCCGA	ACATG					
1450	1460	1470	1480	1490	1500	
AGCTTAACCT	TCGGGAGGGC	GCTTACCACT	TTGTGATTCA	TGACTGGGGT	GAAGTCGTAA	
TCGAATTGGA	AGCCCTCCCG	CGAATGGTGA	AACACTAAGT	ACTGACCCCA	CTTCAGCATT	
1510	1520	1530	1540	1550		
CAAGGTAACC	GTAGGGGAAC	CTGCGGTTGG	ATCACCTCCT	TA.....		
GTTCCATTGG	CATCCCCCTG	GACGCCAACCC	TAGTGGAGGA	AT.....		

FIG. 88D

```

1638 (SEQ ID NO:151)          AGAGTTTGATCCTGGCTCAG
E.colirrSE (SEQ ID NO:158)0 ...AAATTGAAGAGTTTGATCATGGCTCAGATTGAACGGCTGGCGGCAGGCCTAACACATGCA
Cam.jejun5 (SEQ ID NO:159)0 ~TTTTTATGGAGAGTTTGATCCTGGCTCAGAGTGAACGCTGGCGGCTGCTAATACATGCA
Stp.aureus (SEQ ID NO:160)0 ..TTTTATGGAGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCTGCCTAATACATGCA

ER10 (SEQ ID NO:152)
E.colirrSE
Cam.jejun5
Stp.aureus
        GCGGGACGGG
60 AGTCGAACGGTAACAG----GAAGAAGCTTGCTTCTTT----GCTGACGAGTGGCGGACGGG
62 AGTCGAACGAT-----GAAGCTTCTAGCTTGCTAGAGTGA-----TTAGTGGCGCACGGG
61 AGTCGAGCGAA-----CGGACGAGAAAGCTTGCTTCTCTGATG----TT-AGCGGCGGACGGG

TGAGTAA
114 TGAGTAATGTCTGGGA-AACTGCCCTGATGGAGGGGGATAACTACTGGAACGGTAGCTAATA
114 TGAGTAAGGTATAGTTAATCTGCCCTACACAAGAGGACAAACAGTTGGAACGACTGCTAATA
113 TGAGTAACACGTGGATAACCTACCTATAAGACTGGGATAACTTCGGGAACCGGAGCTAATA

175 CCGCATAAC-----GTCGCAAGAC-----CAAAGAGGGGGACCTTCG-GGCCTCTTG
176 CTCTATACTCCTGCTTAACACAAAGTTGAGTAGG-GAAAG-----TTTTT-----CG
175 CCGGATAATAATTTTGAACCGCATGGTTCAAAAGTGAAAGACGGT-----CTT----GCTGTCA

221 CCATCGGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGTAAACGGCTCACCTAGGCGACGA
221 GTGTAGGATGAGACTATATAGTATCAGCTAGTTGGTAAGGTAATGGCTTACCAAGGCTATGA
229 CTTATAGATGGATCCGGCTGCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGA

283 TCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTA
283 CGCTTAACCTGGTCTGAGAGGATGATCAGTCACACTGGAACAGGACACGGTCCAGACTCCTA
291 TACGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACAGGACACGGTCCAGACTCCTA
        ACTCCTA
1659 (COMPL)

```

FIG. 89A

E.colirrsE
Cam.jejun5
Stp.aureus
1659(COMPL)

E.colirrsE
Cam.jejun5
Stp.aureus

E.colirrsE
Cam.jejun5
Stp.aureus

345 CCGGAGGCAGCAGTGGGGAATATTGCACAAATGGGCGCAAGCCCTGATGCAGCCATGCCGCCGTG
345 CCGGAGGCAGCAGTAGGGAATATTGCGCAATGGGGAAACCTTGACGCAGCAACGCCGCCGTG
353 CCGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCCGTG
CGGAGGCAGCAG
407 TATGAAGAAGGCCCTTCGGGTTGTAAAGTACTTTTCAGCGGGGAGGAA-GGGAGTAAAGTTAAT
407 GAGGATGACACTTTTCGGAGCGTAAACTCTTTCTTTAGGGAAG -----AATT
415 AGTGATGAAGGTCTTCGGATCGTAAACTCTGTTATTAGGGAAGACATATGTGTAAGTAAAC
468 ACCTTTGCTCATTGACGTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCCG
455 C-----TGACGGTACCTAAGGAATAAGCACCGGCTAACTCCGTGCCAGCAGCCGCCG
476 -TGTCACATCTTGACGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCCG

FIG. 89B

E.colirrsE	530	GTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTTT
Cam.jejun5	506	GTAATACGGAGGGTGCAAGCGTTACTCGGAATCACTGGGCGTAAAGGGCGCTAGGCGGATT
Stp.aureus	538	GTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCTAGGCGGTTT
E.colirrsE	592	GTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACCTGCATCTGATACTGGCAAGCTT
Cam.jejun5	568	ATCAAGTCTCTTGTGAAATCTAATGGCTTAACCATTAACACTGCTTGGGAACCTGATAGTCTA
Stp.aureus	600	TTTAAGTCTGATGTGAAAGCCACGGCTCAACCGTGGAGGTCATTGGAAACTGGAAACTT
E.colirrsE	654	GAGTCTCGTAGAGGGGGGTAGAAATTCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGA
Cam.jejun5	630	GAGTGAGGGAGAGGCAGATGGAATTGGTGGTGTAGGGGTAAATCCGTAGATATCACCAAGA
Stp.aureus	662	GAGTGCAGAAAGAGGAAAGTGGAATTCATGTGTAGCGGTGAAATGCGCAGAGATATGGAGGA
E.colirrsE	716	ATACCGGTGGCGAAGGCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA
Cam.jejun5	692	ATACCCATTGCCGAAGCGGATCTGCTGGAACCTCAACTGACGCTAAGGCGCGAAAGCGTGGGGA
Stp.aureus	724	ACACCCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACGCTGATGTGCGAAAGCGTGGGGA
E.colirrsE	778	GCAAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGC
Cam.jejun5	754	GCAAACAGGATTAGATACCCCTGGTAGTCCACGCCCTAAACGATGTACACTAGTTGTTGGGGT
Stp.aureus	786	TCAAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGG

FIG. 89C

<i>E.coli</i> rrsE	840	C-CTTGA-GGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGC
<i>Cam. jej</i> un5	816	G-CTAGT-CATCTCAGTAATGCAGCTAACGCATTAAGTGTAACCGCCTGGGGAGTACGGTCGC
<i>Stp.aureus</i>	848	GT-TTCCGCCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCCTGGGGAGTACGACCCG
<i>E.coli</i> rrsE	900	AAGGTTAAAACTCAAATGAATTGACGGGGGCCGACAAAGCGGTGGAGCATGTGGTTTAATT
<i>Cam. jej</i> un5	876	AAGATTAAAACTCAAAGGAATAGACGGGGACCCGCCAAAGCGGTGGAGCATGTGGTTTAATT
<i>Stp.aureus</i>	909	AAGTTGAAACTCAAAGGAATTGACGGGGACCCGCCAAAGCGGTGGAGCATGTGGTTTAATT
<i>E.coli</i> rrsE	962	CGATGCAACGCGAAGAACCTTACCTGGTCTTGACATCCACGGAAGTTTTTCAGAGATGAGAAT
<i>Cam. jej</i> un5	938	CGAAGATACGCGAAGAACCTTACCTGGGCTTGATATCCTAAGAACCCTTTTAGAGATAAGAGG
<i>Stp.aureus</i>	971	CGAAGCAACGCGAAGAACCTTACCAAAATCTTGACATCCTTTGACAACTCTAGAGATAGAGCC
<i>E.coli</i> rrsE	1024	GTG--CCTTCGGG--AA-CCGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTGTGA
<i>Cam. jej</i> un5	1000	GTGCTAGCTTGCTAGAA-CTTAGAGACAGGTGCTGCACGGCTGTCGTCAGCTCGTGTGTGA
<i>Stp.aureus</i>	1033	TTCC-CCTTCGGG--GGACAAAGTGACAGGTGGTGATGGTTGTCGTCAGCTCGTGTGTGA
SB-1		GCAACGAGCGCAACCC
<i>E.coli</i> rrsE	1081	AATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTATCCTTTGTTGCCAGCGGTCCGG-CC
<i>Cam. jej</i> un5	1061	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCACGTATTTAGTTGCTAACGGTTCGG-CC
<i>Stp.aureus</i>	1092	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTAAGCTTAGTTGCCATCA-TTAAGT-T

FIG. 89D

SB-3 (SEQ ID NO:157)		ATGACGTCAAGTCATC
SB-4 (SEQ ID NO:154)		ATGACGTCAAGTCATC
E.colirrsE	1142	GGGAACCTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATC
Cam.jejun5	1122	GAGCACTCTAAATAGACTGCCCTTCG-TAAGGAGGAGGAAGGTGTGGACGACGTCAAGTCATC
Stp.aureus	1152	GGCACTCTAAGTTGACTGCCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATC
SB-3		ATGGCCCTTA
SB-4		ATGGCCCTTACGA
E.colirrsE	1204	ATGGCCCTTACGACCAGGGCTACACACGTGCTACAAATGGCGCATACAAAGAGAAGCGACCTC
Cam.jejun5	1183	ATGGCCCTTATGCCCAAGGCGACACACGTGCTACAAATGGCATATAGAAATGAGACGCAATACC
Stp.aureus	1214	ATGGCCCTTATGATTGGGCTACACACGTGCTACAAATGGACAATACAAAGGCGAGCGAAACC
E.colirrsE	1266	GCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCCAACTCGACTC
Cam.jejun5	1245	GCGAGGTGGAG-CAATCTATAAAATATGTCCCAGTTCGGATTGTTCTCTGCAACTCGAGAG
Stp.aureus	1276	GCGAGGTCAAGCAAATCCCATAAAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTA
E.colirrsE	1328	CATGAAGTCGGAATCGCTAGTAATCGTGGATCAGA-ATGCCACGGTGAATACGTTCCCCGGGC
Cam.jejun5	1306	CATGAAGCCGGAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTGAATACGTTCCCCGGGT
Stp.aureus	1338	CATGAAGCTGGAATCGCTAGTAATCGTAGATCAGC-ATGCTACGGTGAATACGTTCCCCGGGT
1743(compl)		CGGTGAATACGTTCCCCGGGC

FIG. 89E

E.colirrsE	1389	CTTG	TACA	CACG	CCCC	GTCA	CACCAT	GGGAG	TGGG	TGCA	AAAG	AGTAG	GCTTAA	ACCT
Cam.jejun5	1368	CTTG	TACT	CACG	CCCC	GTCA	CACCAT	GGGAG	TGAT	TTCA	CTCG	AAGCCG	GAATAC	T--A-A
Stp.aureus	1399	ATTG	TACA	CACG	CCCC	GTCA	CACCAT	GAGAG	TTTG	TAA	CACCCC	GAAAG	CCGGTGG	GAGTAACCT
1743(compl)		CTTG	TAC											
E.colirrsE	1451	TCG	-GG	AGG	CGCT	TACC	ACTTT	TGTG	ATTCA	TGACT	GGGG	TGAAG	TCGTA	ACAAGGTAACCG
Cam.jejun5	1427	AC	--T	-AG	TTACC	GTCC	ACAG	TGGA	ATCAG	CGACT	GGGG	TGAAG	TCGTA	ACAAGGTAACCG
Stp.aureus	1461	TTA	GGAG	CTAG	CCCG	TCGA	AGGTGG	GACAA	TGATT	GGGG	TGAAG	TCGTA	ACAAGGTAACCG	
E.colirrsE	1512	TAG	GGGA	ACCT	GC	GGT	TGGAT	CACCT	CCCTTA	---				
Cam.jejun5	1485	TAG	GAGAA	ACCT	GC	GGT	TGGAT	CACCT	CCCT	----				
Stp.aureus	1523	TAT	CGGA	AGGT	GC	GGCT	GGAT	CACCT	CCCTTT	CT-				

FIG. 89F

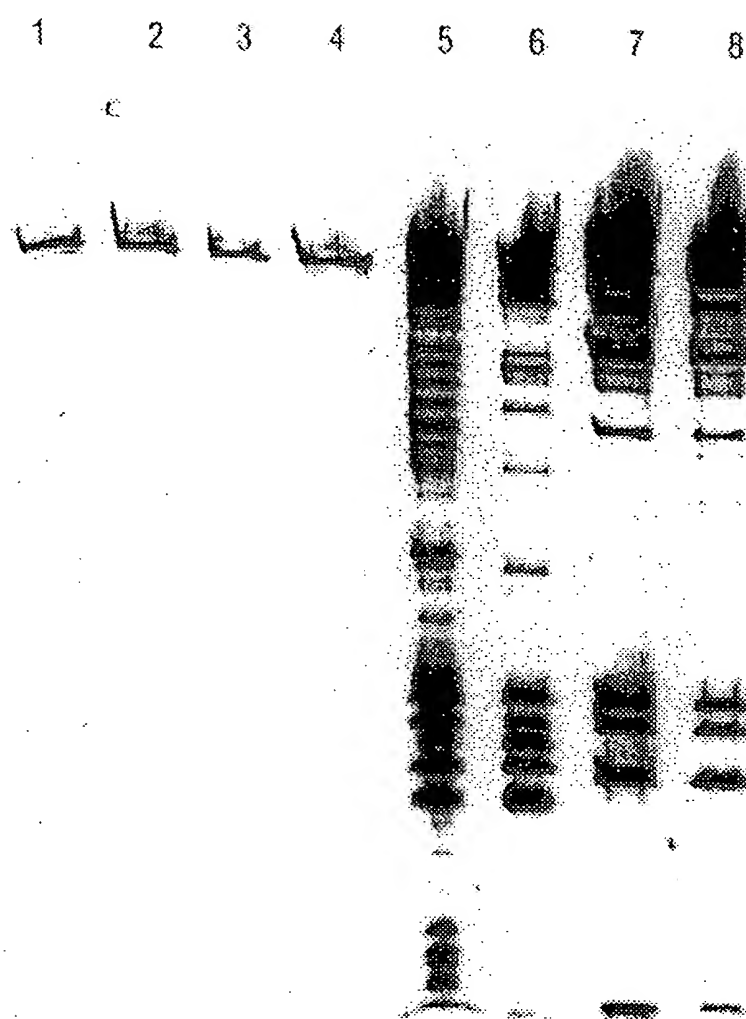


FIG. 90

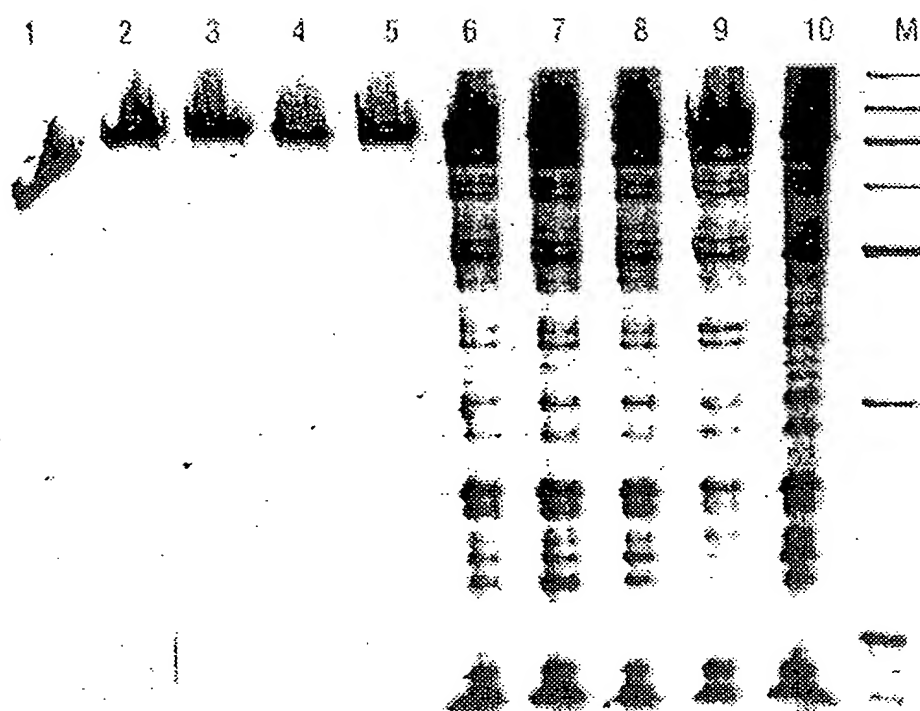


FIG. 91A

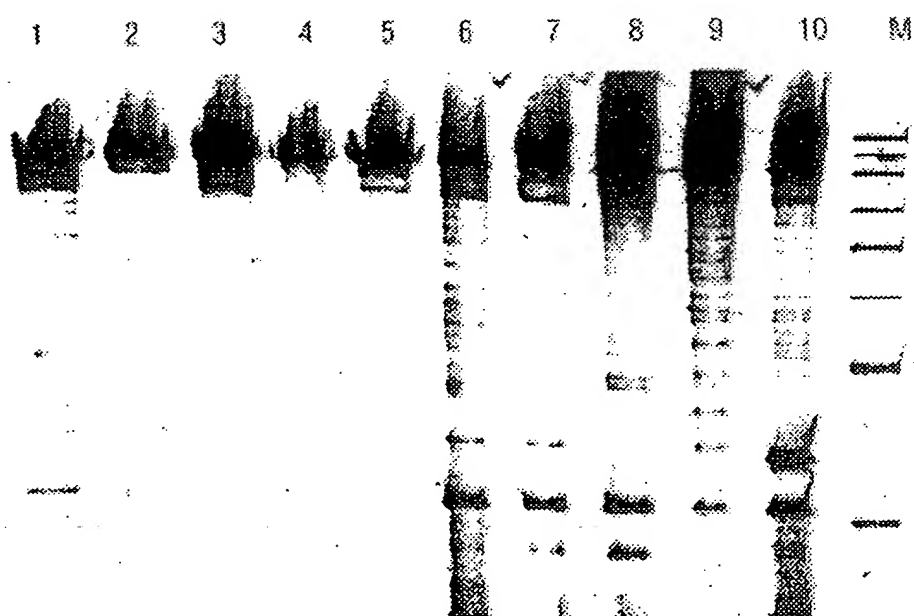


FIG. 91B

1 2 3



FIG. 92



FIG. 93

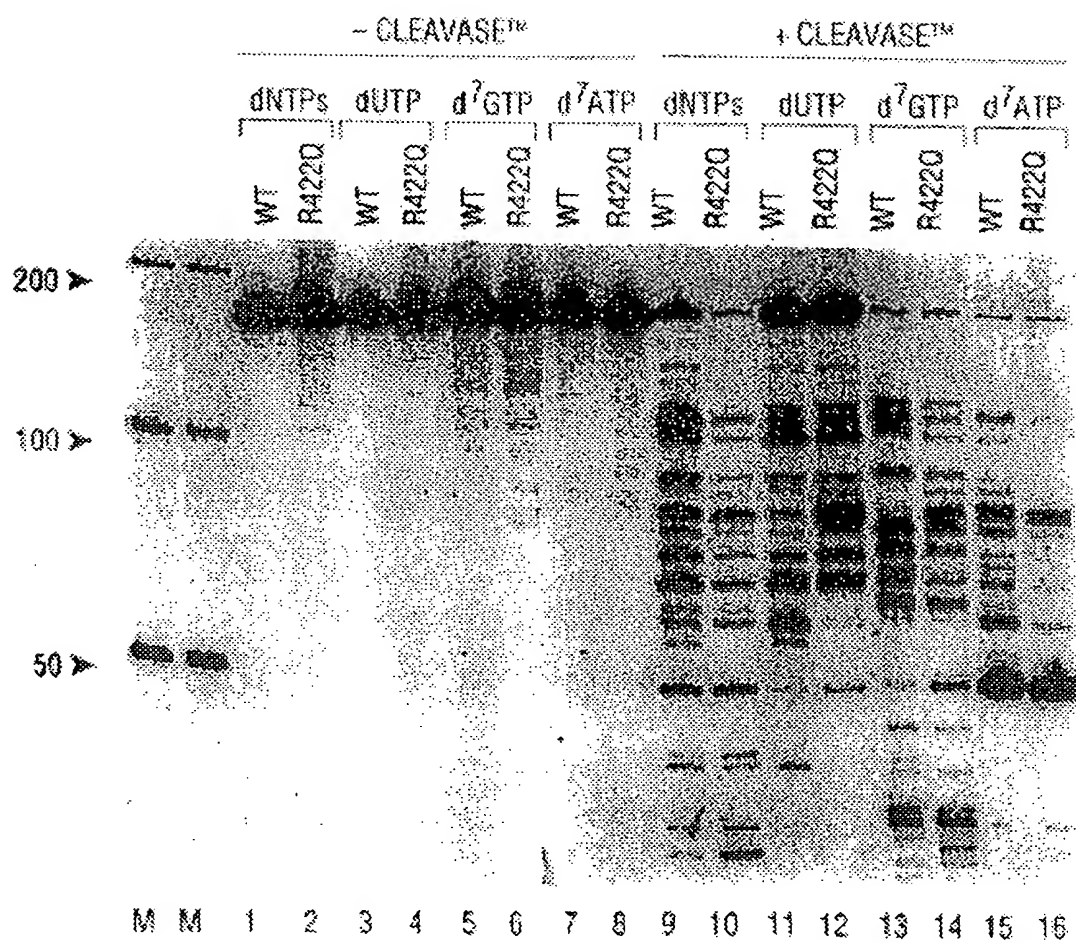


FIG. 94